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STIC-Biotech/ChemLib

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From: Sent: To: Subject: Rao, Manjunath N.

Wednesday, April 18, 2001 3:50 PM STIC-Biotech/ChemLib

Sequence search request for 09/262,126

From: Manjunath N. Rao

Art Unit 1652, Room 10D04

Phone: 306-5681

Date: 4-18-01

Please search the following as soon as possible for application with serial number 09/262,126

SEQ ID NO:. 1 against all nucleic acid databases including issued patents database and pending application database and provide a print of all results.

SEQ ID NO: 2-4 against all protein databases including issued patents database and pending application database. and provide a print of all results.

If you have any questions please call me at the above phone number.

Thanks

Manjunath N. Rao Art Unit 1652 Room CM1, 10D04 Phone 306-5681

Edward Hart Technical Info Specialist STIC / Biotech CM1 12C14 Tel: 305-9203

MANJUNATH N. RAO

Patent Examiner AU 1652, CM1 10D04 703-306-5681

Access DB# 40482

SEARCH REQUEST FORM

Scientific and Technical Information Center

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Requester's Full Name:		Examiner # :	Date:
Art Unit:	Phone Number 30	Serial Number: _	
Mail Box and Bldg/Roon	n Location:	Results Format Preferred (c	ircle): PAPER DISK E-MAIL
If more than one search	h is submitted, please	prioritize searches in order o	of need. **********
Include the elected species or	structures, keywords, synony he any terms that may have a s	describe as specifically as possible the describe as specifically as possible the description of the description of the second meaning. Give examples or relating, and abstract.	and combine with the concept or
Title of Invention:			
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*For Sequence Searches Only appropriate serial number.	Please include all pertinent inj	formation (parent, child, divisional, or is	ssued patent numbers) along with the
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Searches run against the Nucleic Acid Pending database will produce two sets of results, with the extensions .rnpm

Searches run against the Amino Acid Pending database will produce two sets of results, with the extensions .rapm and .rapn

Because they contain data that is confidential, the results of Pending database searches should not be left in the

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Deweer,P. and Amory,A.

Expression system for novel pullulanase patent: US 5736375-A 8 07-APR-1998;

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Deweer,P. and Amory,A.
Expression system for novel pullulanase
Patent: US 5736375-A 9 07-APR-1998;
Location/Qualifiers
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Sequence
ARO44548
                                                                                                                                                                         Unclassified.

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Deweer, P. and Amory, A.
                                                                                                                                              Pullulanase producing microrganisms Patent: US 5817498-A 8 06-OCT-1998; Location/Qualifiers
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180 1429	21 gctgactcttttggagctgttgcaagtgctgatattccaggaaaccccaagtcaggtagga 	Оy

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Deweer,P. and Amory,A.
Pullulanase producing
Patent: US 5817498-A
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3169	TTAATGGCGCTGCTTGGAAAAGACACGATGTCCAAAGCTGCCTCGGAGCTTCATGCTATT	3110	đđ
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3109	ATTATTGATTCCTTAAGTATTGGGTCAATGAGTATCATATTGACGGCTTCCGTTTTGAC	3050	Db
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Deweer, P. and Amory, A.

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Deweer, P. and Amory, A.
Pullulanase, microorganisms which produce
preparation of this pullulanese and the us
Patent: US 6074854-A 9 13-JUN-2000;
Location/Qualifiers
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agaa 13 AGAA 26	LLLLCCALLGACCCLAALLCGGGLALGAAAALGAAGGGAAGTATTTGGCTCTTACA	1321 2570	g 99
tgac 13 TGAC 25	Baacatattacgccaaagaatatagaagatgaggtcatotatgaaatggatgtccgt 	1261 2510	g 9
tgat 12	ggaacgagaggcatgattgtggacctggctaaaacagatcctgctggctg	1201 2450	p 99
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ccat 10	CTTTATGACAGTGCAACGGGTTCTGTAACAAAAATCGTACCTATGACGGCATCGGG	1021 2270	B 8
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TGGT 17	CATGACGACAGCAAATAAGGATATTCCAGTGACATCTGTGAAGGATGCAAGTCT	1670	Db

3889	GACAAATGGGGAAATATCATTGTTGTTGTTATAACCCCAAATAAAAACTGTAGCAACCATCAAT	3830	√ Db
2640	acaaatggggaaatatcattgttgtttataacccaaataaaactgtagcaaccatcaat		γo
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3709	GATTGGAGCAGGAAAGCTCAATATCCAGATGTTTTCAACTATTATAGCGGGCTAATCCAC	3650	DЬ
2460	attggagcaggaaagctcaatatccagatgttttcaactattatagcgggctaatccac	2401	Оу
3649	TCGTANAAAAGGCGGCAACGACAATAGTTATAATGCAGGCGATGCGGTCAATGAGTTT	3590	DЬ
2400	ttcgtanaaaaggcggcaacgacaatagttataatgcaggcgatgcggtcaatgagttt	4	УО
3589	TGTTATGACCTCACAAGGCGTTCCATTCATGCAAGGCGGGAAGAAATG		Дb
2340	cacaagcagttgttatgacctcacaaggcgttccattcatgcaaggcggggaagaaatg	Ñ	γQ
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2280	aaatagccctaagcaatcctaatgattccgaagcggatcggattaaaatggatgaactc	22	Qy
3469	TCTTCACCAGGTGAGACAATTAACTATGTCACAAGTCATGATAACTACACCCTTTGGGAC	3410	дb
2220	cttcaccaggtgagacaattaactatgtcacaagtcatgataactacaccctttgggac	_	γо
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3289	GATCAGCTTCTGACAAAAGGAGCTCAAAAAGGCATGGGAGTAGCGGTGTTTAATGACAAT	3230	90
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3229	ANTCCAGGAATTGCACTTTACGGTGAGCCATGGACGGGTGGAACCTCTGCACTGCCAGAT	3170	đđ
1980	tccaggaattgcactttacggtgagccatggacgggtggaacctctgcactgccagat	9	λồ
3169	TTAATGGCGCTGCTTGGAAAAGACACGATGTCCAAAGCTGCCTCGGAGCTTCATGCTATT	3110	рb
1920	taatggcgctgcttggaaaagacacgatgtccaaagctgcctcggagcttcatgctatt		Ωу
3109	ATTATTGATTCCCTTAAGTATTGGGTCAATGAGTATCATATTGACGGCTTCCGTTTTGAC	3050	ДĠ
1860	ttattgattcccttaagtattgggtcaatgagtatcatattgacggcttccgttttgac	œ	Qy
3049	CCAACGGATCAGGTACTGGAAATGAAATTGCANGCNGAAAGGCCAATGGTTCAAAAATTT	ون	рb
1800	caacggatcaggtactggaaatgaaattgcangcngaaaggccaatggttcaaaaattt	1741	γQ
2989	TCTGACTTCGATAAATTGTACCAGAATATTATTACCGTACGATGATGCAGCTAATTATA	2930	da
1740	cryacttcgatasaattgtaccagaatattattaccgtacgatgatccaggtaattata	1681	γ
2929	.CGTGAACACATTGGGGTTAACATGGATGTTGTCTATAATCATACCTTTGCCACGCAAATC	æ	Db
1680	gtgaacacattggggttaacatggatgttgtctataatcatacctttgccacgcaaatc	1621	γQ
2869	AGAAATGCGAATGCTCGTATAAAAGAGTTTAAGGAAATGGTTCTTTCACTCCAT	2810	ДĎ
1620	aaatgcgaatggtaatgctcgtataaaagagtttaaggaaatggttctttcactccat	1561	Qγ

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Deweer,P. and Amory,A.

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            acaaatgcgaatggtaatgctcgtataaaagagtttaaggaaatggttcttttcactccat
       ACAAATGCGAATGGTAATGCTCGTATAAAAGGGTTTAAGGAAATGGTTCTTTCACTCCAT
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Deweer,P. and Amory,A.

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VERSION KEYWORDS	DEFINITION ACCESSION	A38130	RESULT 15
A38130.1	Sequence A38130	0 t 18 t 4	
GI:2294741	Sequence 10 from Patent EP0605040 A38130	2784 hp	
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Deweer, P. and Amory, A.

Pullulanase, micro-organisms producing the preparation thereof as well as its use patent; EP 0605040-A 10 06-JUL-1994;

SOLVAY (BE)

Other publication JP 6217770 940809

Other publication CA 2112028 940829

Other publication CN 1090325 940803

Other publication CN 1090325 940803

Other publication BE 1007523 951010

Other publication BE 1007723 950516

Other publication BE 1007733 950516

Other publication BE 100783 940913.
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2340	81 gcacaagcagttgttatgacctcacaaggcgttccattcatgcaaggcgggggaagaaatg 	228
2280	21 aabatagccctaagcaatcctbatgattccgaagcggatcggat	222
2220	61 tottcaccaggtgagacaattaactatgtcacaagtcatgataactacaccctttgggac 	216: 216:
2160 2160	01 gcaacaggottaactgatgcaattaagaatggcgttgaggggagtattaatgactttacc 	210: 210:
2100 2100	1 ttacgaaacgcgttggac 	204
2040	81 gatcagettetgacaaaaggageteaaaaaggeatgggagtageggtgtttaatgacaat 	198: 198:
1980	21 aatccaggaattgcactttacggtgagccatggaagggtggaacctctgcactgccagat 	192: 192:
1920	61 ttaatggcgcTgcTTgGAAAAGACACGATgTCCAAAGCTGCCTCGGAGCTTCATGCTAFT	186
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76.2 2.7 1993 18 T93875 Z 76.2 2.7 2094 20 V65118 C 74.4 2.7 5058 20 X91106 G 74.4 2.7 5058 20 X91106 G 73.6 2.6 784 20 X33179 G 73.6 2.6 784 20 X33179 72.2 2.6 2646 16 T02400 R 72.2 2.6 2982 16 T02400 R 72.2 2.6 2982 17 T31478 S 68.2 2.4 3437 17 T31478 S 53.6 1.9 273254 21 C81914 S 53.6 1.9 273254 21 C81914 C 53.6 1.9 273254 21 C81914 C 53.6 1.9 273254 21 V237061 R 48 4133 9 W81341 C 47.6 1.7 2244 17 T10429 M 47.6 1.7 2244 17 T10429 M 47.6 1.7 2344 19 V23640 F 45.2 1.6 1663 20 X3636 M 45.2 1.6 1663 20 X37066 M 45.2 1.6 1663 20 X37066 D 45.2 1.6 1038602 20 Z01425 P 43.4 1.6 1286 20 X34624 P 43.4 1.6 2235 10 W90389 F 42.6 1.5 6142 17 T47878 B 39.6 1.4 2843 20 V62881 F 5	iginal S.	X27065	20	2843	1.4	39.4	44
76.2 2.7 1993 18 T93875 Z 76.2 2.7 2904 20 V65118 C 74.4 2.7 5058 20 X91106 G 74.4 2.7 5058 20 X91106 G 73.6 2.6 784 20 X33179 G 73.6 2.6 784 20 X33179 72.2 2.6 2942 16 T02400 R 72.2 2.6 2982 16 T02400 R 72.2 2.6 2982 17 T31478 S 53.6 1.9 273254 21 C81914 S 53.6 1.9 273254 21 C81914 C 53.6 1.9 273254 21 C81914 C 53.6 1.9 273254 21 C81914 C 52 1.9 2133 18 T96754 S 52 1.9 2133 18 T96754 S 52 1.9 2706 20 X27061 R 48 1.7 624 20 V65116 C 47.6 1.7 2344 17 T10429 F 47.6 1.7 2334 19 V23639 M 47.6 1.7 2334 19 V23639 M 45.6 1.6 1663 20 X33162 C 45.2 1.6 103860 20 X33162 C 45.2 1.6 103860 20 X34654 C 45.4 1.6 103860 20 X34654 C 45.4 1.6 2337 10 N91089 F 43.4 1.6 2337 10 N91089 F 43.4 1.6 3337 10 N91089 F 42.2 1.5 6142 27 T47878 B 42.2 1.5 6142 27 T67881 F 58.4 2949 21 D00024	S. tuberosum isoam	x27060	20	2843	1.4	39.4	43
76.2 2.7 1993 18 T93875 Z 76.2 2.7 1993 78 T93875 Z 74.4 2.7 5058 20 X91106 73.6 2.6 784 20 X33179 72.8 2.6 2645 16 T02400 72.2 2.6 2982 16 T02400 72.2 2.6 2982 16 T02399 68.2 2.4 3437 17 T31478 53.6 1.9 273254 21 C81914 53.6 1.9 273254 21 C81914 53.6 1.9 273254 21 C8194 49 1.8 4133 9 N81341 49 1.8 4133 9 N81341 47.6 1.7 2244 17 T10429 47.6 1.7 2244 19 V23640 47.6 1.7 2244 19 V23640 47.6 1.7 2344 19 V23640 47.6 1.6 1860 21 A56836 45.2 1.6 1638602 20 X31623 45.2 1.6 1038602 20 X31624 45.4 1.6 1706 20 X21066 45.4 1.6 1706 20 X21085 43.4 1.6 2335 10 N90389 43.4 1.6 2335 10 N90389 43.4 1.6 3337 10 N91089 42.2 1.5 6142 20 V62881	Degenerate DNA enc	D00024	21	2949	1.4	39.6	42
76.2 2.7 1993 18 T93875 Z 76.2 2.7 2904 20 V65118 C 74.4 2.7 5058 20 X91106 G 74.4 2.7 5058 20 X3179 G 73.6 2.6 784 20 X3179 72.8 2.6 3753 21 A05807 R 72.2 2.6 2646 16 T02400 R 72.2 2.6 2982 16 T02400 R 72.2 2.6 2982 17 T31478 S 53.6 1.9 273254 21 C81914 S 53.6 1.9 273254 21 C81914 C 53.6 1.9 273254 21 C81914 C 53.6 1.9 273254 21 C81914 C 53.6 1.9 273254 21 T10429 R 52 1.9 2133 18 T95754 S 52 1.9 2706 20 X27061 R 647.6 1.7 2244 17 T10429 M 647.6 1.7 2344 17 T10428 F 647.6 1.7 2344 19 V23639 F 645.2 1.6 1860 21 X56836 F 645.2 1.6 1860 20 X27066 S 645.2 1.6 103860 20 X27066 S 645.4 1.6 103860 20 X33162 S 645.4 1.6 103860 20 X30163 S 645.4 1.6 103860 20 X30163 S 645.4 1.6 2235 10 N90389 F 647.6 1.5 3337 10 N90389 F 647.6 1.5 3337 10 N90389 F 647.6 1.5 3397 21 Z24492 W 647.6 1.5 5642 17 T47878 B	Full length Pull	V62881	20	6142	1.5	42.2	41
76.2 2.7 1993 18 T93875 Z 76.2 2.7 2904 20 V65118 C 74.4 2.7 5058 20 X91106 G 74.4 2.7 5058 20 X91106 G 73.6 2.6 784 20 X33179 G 73.6 2.6 784 20 X33179 72.2 2.6 2982 16 T02405 R 72.2 2.6 2982 16 T02405 R 72.2 2.6 2982 17 T31478 C 53.6 1.9 273254 21 C81914 S 53.6 1.9 273254 21 C81914 C 53.6 1.9 27325 20 V27061 R 48 1.7 6243 20 V27061 C 47.6 1.7 2244 17 T10429 F 47.6 1.7 2334 19 V23639 F 47.6 1.7 2334 19 V23639 M 48.1 1.6 1860 20 X33162 C 45.2 1.6 1860 20 X33162 C 45.2 1.6 103860 20 X33162 C 43.4 1.6 1706 20 X34654 D 43.4 1.6 2337 10 N90389 F 43.4 1.6 2337 10 N90389 F 43.6 1.5 2997 21 Z24492 W	Bacillus alkaline	T47878	17	6142	1.5	42.2	40
76.2 2.7 1993 18 T93875 Z 76.2 2.7 1994 20 V65118 C 74.4 2.7 5058 20 X91106 G 73.6 2.6 784 20 X33179 73.6 2.6 784 20 X33179 72.2 2.6 2646 16 T02400 R 72.2 2.6 2982 16 T02400 R 72.2 2.6 2982 16 T02399 68.2 2.4 3437 17 T31478 S 53.6 1.9 273254 21 C81914 53.6 1.9 1230025 20 X91990 53.6 1.9 1230025 20 X91990 53.6 1.9 27354 21 T96754 S 52 1.9 2735 18 T96754 S 52 1.9 2706 20 X29061 Re 49 1.8 4133 9 N81341 C 47.6 1.7 2244 19 V23640 M 47.6 1.7 2244 19 V23640 M 47.6 1.7 2334 17 T10428 M 47.6 1.7 2334 17 T10428 M 47.6 1.7 2334 19 V23639 F 45.2 1.6 1860 20 X27066 45.2 1.6 2806 20 X2065 45.2 1.6 1038602 20 X3162 43.4 1.6 1038602 20 Z01425 43.4 1.6 3337 10 N91089 F	~	Z24492	21	2997	1.5	42.6	39
76.2 2.7 1993 18 T93875 Z 76.2 2.7 2994 20 V65118 C 74.4 2.7 5058 20 X91106 G 73.6 2.6 784 20 X33179 G 73.6 2.6 784 20 X33179 G 73.6 2.6 2646 16 T02400 R 72.2 2.6 2982 16 T02400 R 72.2 2.6 2982 16 T02399 R 68.2 2.4 3437 17 T31478 S 53.6 1.9 273254 21 C81914 G 53.6 1.9 1230025 20 X91990 S 52 1.9 2133 18 T96754 S 52 1.9 2133 18 T96754 S 52 1.9 2136 20 X27061 R 48 11.7 2244 17 T10429 M 47.6 1.7 2244 17 T10429 M 47.6 1.7 2244 19 V23640 M 47.6 1.7 2344 19 V23640 M 48.6 1.6 2334 17 T10428 F 45.2 1.6 1860 21 X56836 F 45.2 1.6 1860 20 X3162 P 45.2 1.6 1038602 20 X27066 43.4 1.6 1038602 20 X304654 P 43.4 1.6 2235 10 N90389 D	Fragment of Pseudo	N91089	10	3337	1.6	43.4	38
76.2 2.7 1993 18 T93875 Z 76.2 2.7 2904 20 V65118 C 74.4 2.7 5058 20 X91106 G 74.4 2.7 5058 20 X3179 G 73.6 2.6 784 20 X33179 G 72.2 2.6 2646 16 T02405 R 72.2 2.6 2982 16 T02405 R 72.2 2.6 2982 17 T31478 S 68.2 2.4 3437 17 T31478 S 53.6 1.9 273254 21 C81914 S 53.6 1.9 273254 21 C81914 C 53.6 1.9 273254 21 C81914 S 52 1.9 2133 18 T96754 S 52 1.9 2133 18 T96754 S 52 1.9 2106 20 X27061 R 48 1.7 2244 17 T10429 R 47.6 1.7 2344 17 T10429 F 47.6 1.7 2344 17 T10428 I 47.6 1.7 2344 19 V23639 F 47.6 1.7 2344 19 V23639 F 45.2 1.6 1863 20 X33162 P 45.2 1.6 1863 20 X33162 P 43.4 1.6 1706 20 X34654 P	DNA encoding pol	N90389	10	2235	1.6	43.4	37
76.2 2.7 1993 18 T93875 Z 76.2 2.7 1993 20 V65118 C 74.4 2.7 5058 20 X91106 G 73.6 2.6 784 20 X3179 G 73.6 2.6 3753 21 A05807 G 72.2 2.6 2945 16 T02400 R 72.2 2.6 2982 16 T02400 P 72.2 2.6 2982 17 T31478 S 53.6 1.9 273254 21 C81914 C 53.6 1.9 1230025 20 X91990 S 52 1.9 273254 21 C81914 C 53 6 1.9 1230025 20 X91990 S 52 1.9 27354 21 T96754 S 52 1.9 2736 20 X27061 S 49 1.8 4133 9 N81341 Re 47.6 1.7 2244 17 T10429 M 47.6 1.7 2244 19 V23649 F 47.6 1.7 2344 19 V23639 F 47.6 1.7 2344 19 V23639 F 48.6 1.6 1860 20 X270166 O 45.2 1.6 2806 20 X270166	Partial cDNA for	X34654	20	1706	1.6		36
76.2 2.7 1993 18 T93875 Z 76.2 2.7 2904 20 V65118 C 74.4 2.7 5058 20 X91106 G 73.6 2.6 784 20 X33179 G 73.6 2.6 784 20 X33179 G 73.6 2.6 3753 21 A05807 G 72.2 2.6 2646 16 T02400 R 72.2 2.6 2982 16 T02400 R 72.2 2.6 2982 16 T02399 R 68.2 2.4 3437 17 T31478 S 53.6 1.9 273254 21 C81914 C 53.6 1.9 1230025 20 X91990 S 53.6 1.9 273254 21 C81914 C 53.6 1.9 273254 21 C81914 C 53.6 1.9 273254 21 C8194 C 53.6 1.7 2244 12 V23640 R 49 1.8 4133 9 V81341 C 47.6 1.7 2244 19 V23640 M 47.6 1.7 2244 19 V23640 I 47.6 1.7 2344 19 V23640 I 48.6 1.6 234 19 V23649 F 48.6 1.6 1860 21 A56836 F 45.2 1.6 2806 20 X27066		201425	20	1038602	1.6	45	35
76.2 2.7 1993 18 T93875 Z 76.2 2.7 2904 20 V65118 C 74.4 2.7 5058 20 X91106 G 74.4 2.7 5058 20 X3179 G 73.6 2.6 784 20 X33179 G 73.6 2.6 784 20 X33179 G 72.2 2.6 2946 16 T02405 R 72.2 2.6 2982 16 T02405 R 68.2 2.4 3437 17 T31478 S 53.6 1.9 273254 21 C81914 S 53.6 1.9 273254 21 C81914 S 53.6 1.9 273254 21 C81914 S 52 1.9 273254 21 C81914 S 52 1.9 273254 21 T31478 S 52 1.9 27365 20 X27061 S 52 1.9 2133 18 T96754 S 52 1.9 2133 18 T96754 S 52 1.9 2133 18 T96754 S 52 1.9 2706 20 X27061 R 64 1.7 2244 17 T10429 R 64 7.6 1.7 2344 17 T10429 F 64 7.6 1.7 2344 17 T10428 F 64 7.6 1.7 2344 19 V23639 F 65 1.6 186 21 A56836 M 65 1.6 1863 20 X33162 F 65 1.6 1863 20 X33162	Original S. tubero	X27066	20	2806	1.6	45.2	34
76.2 2.7 1993 18 T93875 Z 76.2 2.7 1994 20 V65118 C 74.4 2.7 5058 20 X91106 G 73.6 2.6 784 20 X33179 G 73.6 2.6 784 20 X33179 G 73.2 2.6 2646 16 T02400 R 72.2 2.6 2982 16 T02400 P 72.2 2.6 2982 16 T02399 G 72.2 2.6 2988 16 T02399 S 68.2 2.4 3487 17 T31478 S 53.6 1.9 273254 21 C81914 C 53.6 1.9 1230025 20 X91990 S 52 1.9 27354 21 C81914 C 53 1.9 27354 21 T96754 S 52 1.9 2733 18 T96754 S 52 1.9 2736 20 X27061 S 49 1.8 4133 9 N81341 Re 47.6 1.7 2244 17 T10428 M 47.6 1.7 2344 19 V23639 F 47.6 1.7 2334 17 T10428 F 48.6 1.6 2712 20 X76375 E	Potato isoamylas	X33162	20	1663	1.6	45.2	33
76.2 2.7 1993 18 T93875 Z 76.2 2.7 1994 20 V65118 C 74.4 2.7 5058 20 X91106 G 73.6 2.6 784 20 X33179 72.8 2.6 3753 21 A05807 G 72.2 2.6 2646 16 T022405 R 72.2 2.6 2982 16 T022400 P 72.2 2.6 2982 16 T02399 R 68.2 2.4 3437 17 T31478 S 53.6 1.9 273254 21 C81914 C 53.6 1.9 1230025 20 X91990 S 52 1.9 27354 21 T96754 S 52 1.9 2736 20 X91990 S 53 1.9 2736 20 X91990 S 68 2 2.4 347 17 T10428 R 68 1.7 2244 19 V23640 M 67.6 1.7 2244 19 V23640 M 67.6 1.7 2334 19 V23639 F 68 1.6 1860 21 A56836 M	Zea mays SU1 star	X76375	20	2712	1.6	45.6	32
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76.2 2.7 1993 18 T93875 Z 76.2 2.7 1994 20 V65118 C 74.4 2.7 5058 20 X91106 G 73.6 2.6 784 20 X33179 G 73.8 2.6 3753 21 A05807 G 72.2 2.6 2982 16 T02400 R 72.2 2.6 2982 16 T02400 P 72.2 2.6 2982 16 T02399 S 72.2 2.6 2983 17 T31478 S 53.6 1.9 273254 21 C81914 C 53.6 1.9 273254 20 X27061 S 62 1.9 2706 20 X27061 S 64 1.7 2244 17 T10428 Rec 67.6 1.7 2244 19 V23640 F 68 1.7 2244 17 T10428 F	Full length Flavo	V23639	19	2334	1.7		30
76.2 2.7 1993 18 T93875 Z 76.2 2.7 1994 20 V65118 C 74.4 2.7 5058 20 X91106 G 73.6 2.6 784 20 X33179 G 73.6 2.6 784 20 X33179 G 73.2 2.6 2646 16 T02400 R 72.2 2.6 2982 16 T02400 P 72.2 2.6 2982 16 T02399 G 72.2 2.6 2982 16 T02399 S 53.6 1.9 273254 21 C81914 C 53.6 1.9 1230025 20 X91990 S 52 1.9 273254 21 T93478 S 52 1.9 273254 21 T96754 S 52 1.9 273264 S 53 1.9 2736 20 X27061 S 54 1.8 4133 9 N81341 Re 64 1.7 2244 19 V23640 F	Isoamylase gene.	T10428	17	2334	1.7		29
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76.2 2.7 1993 18 T93875 Z. mays. 76.2 2.7 2904 20 V65118 Corn pul. 74.4 2.7 5058 20 X91106 Group B 73.6 2.6 784 20 X33179 Pullana. 72.8 2.6 3753 21 A05807 Group B 72.2 2.6 2646 16 T02400 Pullulan.	Rice mature pull	T02399	16	2988	6	۲	19
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		T93875	18		2.7	ა	12

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ALIGNMENTS

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RESULT
X87941
Miller BS, Shetty JK;
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                      (GEMV ) GENENCOR INT INC
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                                                                                                                                                                                                                                                      X87941;
                                        04-MAR-1998;
                                                         03-MAR-1999;
                                                                                                                                                                                                                   Bacillus deramificans mature pullulanase coding sequence.
                                                                          10-SEP-1999
                                                                                           WO9945124-A2
                                                                                                                                                                Bacillus deramificans.
                                                                                                                                                                                                                                                                     X87941 standard; DNA; 2794 BP.
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                                        98US-0034630
                                                         99WO-US04627
                                                                                                                                      Location/Qualifiers
1..2787
                                                                                                           /EC_number= "3.2.1.41"
/product= "pullulanase"
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P-PSDB;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents Bacillus deramificans strain CC T89 117D DNA coding for mature pullulanase (EC-3.2.1.41). This CC enzyme has a pl of 4.1-4.5, has a half-life of about 55 hr at 60 CC deg C and 1s capable of catalysing the hydrolysis of CC deg C and 1s capable of catalysing the hydrolysis of CC invention relates to the discovery that B. deramificans pullulanase recombinantly produced in a Bacillus host is modified yet retains CC the ability to catalyse the hydrolysis of an alpha-1,6-glucosidic bond. The modification of the recombinant pullulanase appears to be a result of misprocessing of the signal sequence by a signal cC peptidase as well as susceptibility to extracellular proteclytic CC processing. The invention provides modified pullulanases, nucleic acids encoding them, vectors, host cells and methods for CC the starch industry for the saccharification of aqueous liquefied starch, forming syrups of high glucose and maltose content. Other uses (not claimed) are: as anti-staling additives in bread; in the preparation of oligosaccharides from amylopectin or of the proparation of oligosaccharides from amylopectin or of tertaholosides from maltose; to condense mono or oligosaccharides, cor in the pharmaceutical industry (no details). When used for custoris as short reaction times, without losses associated with corrects on reaction products, especially they provide higher glucose contents of by-products, especially they provide higher glucose contents of the pharmaceutical industry (no details). When used for exercision reaction products, without losses associated with the pharmaceutical industry (no details) in the material contents of dissolved solids in the material contents of signal products of dissolved solids in the material contents of contents of the process.
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15-JUL-1993;
19-NOV-1993;
                                                                                                                                             This sequence codes for the mature pullulanase enzyme isolated from Bacillus deramificans 7 89.117D. The pullulanase hydrolyses the alpha-1,6-glycosidic bonds of amylopectin and of pullulan. The enzyme can be used (with glucoamylase) for saccharification of starch. Typical applications include use as anti-staling additives in bread making and brewing, in preparation of low calorie foods and to clarify fruit juices.
                                                                                                                                                                                                                              New pullulanase from Bacillus deramificans - 1 saccharification etc., with good stability over ranges, also related DNA vectors, transformed
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74	totgacttogataaasttgtaccagaatattattaccgtacgatgatgcaggtaattata	68	B 7
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1380	tttccattgaccctaattcgggtatgaaaaataaagggaagtatttggctcttacagaa :	1321	фq
1380	tttccattgaccctaattcgggtatgaaaaataaagggaagtatttggctcttacaga		Qy
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                              The present sequence encodes a trimmed enzyme isolated from Bacillus sp. APC-9603. The present specification also describes: (1) a vector containing the DNA encoding a trimmed enzyme; (2) a recombinant microbe transformed by the DNA; and (3) preparation of a trimmed enzyme in which the microbe of (2) is cultured and the trimmed enzyme is collected from the culture. The method can prepare a trimmed enzyme of wide substrate specificity having heat resistance and being active in acid region efficiently.
Sequence
                                                                                                                                                                                                                               Claim
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••
  3934 BP;
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1200 A; 756 C;
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908 G; 1070 T;
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БР В 밁 Qy 멍 В δõ Ş 밁 Ş Ş 밁 Q 밁 Š Q 밁 Q γ 멅 밁 Q 밁 Q δÃ 밁 οy Query Match Best Local S Matches 2208 1227 1167 1107 1047 1284 781 661 601 541 721 481 987 421 927 361 867 301 807 241 747 181 687 121 630 570 61 Local Similarity mes 2208; Conserv <u>بــا</u> attatogttogcaotcaagattggaccaaagatgtgagcgctgaccgctacatagattta gatgggaacacgacaacgatcattgtccactatttttgccctgctggtgattatcaacct 60 ttacaagtaga---aagcggggttaaaacggatctcgtgacggttactctagggggaagat ttttcgtatattccgtccactcatgcagtctatgacacaattaataatcctaatgcggat cogagttacccatctgacaacattaatttaacagtccctgccggcggtgcacacgtcact gcacctgataatcatagtacgcagcttaaaaaagtaaatgataacctttaccaattttcc gcacctgataatcacagtactttattaaaaaaggtgactaacaatctctatcaattctca cacgatgacactgcaaatggggatatcccggttactaaggtgaagaatgccaataaggtc catgacgacacagcaaataaggatattccagtgacatctgtgaaggatgcaagtcttggt gatgctgaggatgcagctaaacccgctgtaagcaacgcttatttagatgcttcaaaccag agcaaaggaaatgaggtgtggcttgtagaaggaaacagccaaattttttataatgaaaaa gctgactcttttggagctgttgcaagtgctgatattccaggaaacccaagtcaggtagga tggagtctatggatgtggccaaaagacggaggtggggctgaatacgatttcaatccg gacggaacgacaacaaacgtcattgttcattattttcggccaggtggtgattaccaatca ttctcttatgtcccgtccacccatgctgtatatgacacgattaataatccaggagctaat gatgctgaagatgccgccgagcccgctgtgagcaatgcttatttagatgcgccaaataag agcaaaggtcatgaggtttggcttgtccagggaaatagccaaattttttataatgaaaag attattgttcgcacccaggattgggcaaaagatgtgagtcaagaccgctacatagatctt acagattcgtatggggaaattgccaatgtttcgattccagggagtccaagtaaggttgga tggagtctttggatgtggccagaaggtggtgatgggaacaattataattttaatgga----agctacccatctgacaacattaatttaactgtaccggatggaggcgcacatgtgacg Conservative 65.3%; 0 Score 1823 Pred. No. Mismatches 0.6; 544; DΒ 19; Indels Length Gaps 1283 837 1343 660 1046 480 420 866 746 989 120 629 600 986 360 806 240 780 540 300

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Pullulanase; genetically

pulB; debranching e
engineered variant;

enzyme; ; wheat; sequence

amylopectin; potato; wheat

thermostable;

corn;

Pullulanase 05-MAY-2000

(pulB)

nucleotide entry) Z89960

standard;

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RESULT
Z89960
ID Z8
XX
XX
AC Z8
AC Z8
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AC P1
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Best Local Similarity 66.7%;
Matches 1305; Conservative
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Matches 933;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glycosidase enzymes from organisms of the genera Staphlothermus, Pyrococcus and Thermococcus - for deriving sugar from oligosaccharides, useful in the e.g. food processing, textile or
     1163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dairy products, fruit juice, detergent, textile, guar gum, animal feed, plant biomass or waste product) containing oligosaccharides (selected from maltose, celloblose, lactose, sucrose, raffinose, starchyose, verbascose, cellulose, starch, amylose, glycogen, disaccharides, polysaccharides and pullulan) with one of the claimed of the contained of the claimed of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (6GP3) that grows optimally at 85 degC. The sequence shows 53% nucleic acid identity to an alpha destrom 6 glucanohydrolase of
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New thermostable glycosidase(s) -
                                                Bylina
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11-JAN-1996;
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llarity 50.7%;
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Pred. No. 6.2e-68;
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                                                                  (NISO ) NIPPON SHOKUHIN KAKO
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(SHKJ ) SHINGIJUTSU JIGYODAN.
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                             tgacaaaaggagctcaaaaaggcatgggagtagcggtgtttaatgacaatttacgaaacg
                                                             tccttgtgtatgggcaagggtgggatttgccgacgctcttccaccggaacattaggcgac
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Pred. No. 3.5e-55;
0; Mismatches 653;
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                                             Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays pharmaceutical compositions and vaccines for Streptococcus
        Claim 1; Page 900-906; 1409pp; English
                                                                                                                                                                                                                                                                                                                      Streptococcus pneumonlae; computer readable medium;
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                                                                                                                          Choi GH,
Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                            pneumoniae
                                                                                                                                                                                                                                                                                                                                                            pneumoniae genome fragment SEQ ID NO:132
                                                                                                                                                                                        96US-0029960
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                                                                                                                                         Dillon
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                                                                                                                                                                                                                                                                                                                      vaccine; pharmaceutical composition;
                                                                                                                                                                                                                                                                                                                                    S. pneumoniae; genome; diagnosis;
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composition in the present invention also describes an isolated nucleic acid conclude encoding a homologue of any of the fragments of the S.pneumoniae genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced by a process comprising: (a) screening a genomic DNA library using as a comprise a target sequence defined by any of the sequences in SEQ ID NO:1 to 391, identifying members of the library which contain sequences at that hybridise to the target sequence and isolating the nucleic acid concludes from the members; or (b) isolating mRNA, DNA or cDNA produced from an organism, amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification primers derived from the concent of the S. pneumoniae genome to prime the amplification and isolating the amplified sequences. The computer readable medium can be used in a computer-based system for identifying fragments of the S. pneumoniae genome. Products from the present compositions and vaccines for S. pneumoniae, and pharmaceutical compositions and vaccines for S. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a computer readable medium which has the nucleotide sequences SEQ ID NO:1 to 391 (V52134 to V55524) recorded on it, or a representative fragment or a sequence at least 95% identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEQ ID NO: 1 to 391 (V52134 to V52524) are genomic fragments from Streptococcus
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Sequence 9541 BP; 2886 A; 2081 C; 1691 G; 2883 T; 0 other;

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                                      atggcgctgcttggaaaagacacgatgtccaaagctgcctcggagcttcatgctattaat 1923
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57; Conservative
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0; Mismatches 518
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                                        WPI; 1997-458572/43.
P-PSDB; W34878.
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 mays debranching

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          starch
                   DNA encoding maize de-branching enzyme -
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/product= debranching enzyme
/note= "partial coding sequence"
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                                                                                                                                                                                                                                                                                          maize;
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                    useful for production
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RESULT 13
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Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence encodes a novel debranching enzyme isolated from 2em mays (maize). This enzyme has been used in the production of transgenic plants in which the nucleic acid is stably integrated into the host cell's genome and expressed. Such an enzyme can be used in the production of starch which is useful in the food industry or in the production of industrial products e.g. paper, adhesives, textiles, textile care products, building materials, soil stabilisers, agrochemicals, pharmaceutical products, cosmetics, coal briquettes, flocculants for parameteristics and coal surries, foundry sand binders, rubber goods, leather
                                                                                                                                                                                                                                                                                                                                                                                                                   1851
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                                                                                                                                                           Corn pullulanase cDNA fragment
                                                                                                                                                                                          02-MAR-1999
                                                                                                                                                                                                                                                   V65118
                                                                                                                                                                                                                                                                                                                                                       1911 tcatgctatta
                          12-NOV-1998
                                                                                   Zea mays
                                                                                                                            Pullulanase; corn; transgenic plant; starch structure; isolation;
                                                       WO9850562-A1
                                                                                                                 screening;
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                                                                                                                                                                                                                                                   standard;
                                                                                                                 developmental stage;
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Pred. No. 8.
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Best Local :
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                15-NOV-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ccaagataattggggttatgaccctcgcaactatgatgttcctgaagggcagtatgctac 1562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence encodes a fragment of a novel Zea mays pullulanase
                                                                                                                                                                                                        tcaaaaatttattattgattcccttaagtattgggtcaatgagtatcatattgacggctt
                                                                                                                                                                                                                                                                                            aatggtcagactgagaacagcgcggctgtgaacaatacagcaagtgagcatttc-atggt
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                                                                  standard;
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             (first entry)
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                                                                  DNA;
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Pred. No. 1
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le-11;
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                                                                                                                                                                                                  can be recombinantly expressed using standard recombinant methodology. The GBS antigens of the invention can be used as vaccine components for the treatment or prophylaxis of diseases and symptoms mediated by Streptococcus infection, especially group A Streptococcus (S. pyogenes), GBS or S. agalactiae, S. dysgalactiae, S. uberis, S. nocardia, as well as Staphylococcus aureus. The vaccines are administered to those individuals at risk of GBS infection, particularly pregnant women and infants for sepsis, meningitis, and pneumonia, as well as immunocompromised individuals, such as those with diabetes, liver disease or cancer. The vaccines also have vetinary applications, such as for the treatment of mastitis in cattle. The present sequence represents a DNA encoding 4
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                                                                1508 ataattggggttatgaccctcgcaactatgatgttcctgaagggcagtatgctacaaatg 1567
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                                                                                                                                                                 Sequence 5058 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                     Novel group B Streptococcus antigens -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Boyer
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                                                                                                                                                                                          antigens
                                                                                                                                                                                                                                                                                                                                             invention provides Group B Streptococcus nucleic acids (X91103-X91111) encoding the
                      cgaatggt---aatgctcgtataaaagagtttaaggaaatggttctttcactccatcgtg 1624
caaaagatccatcagcacgtatcgccgaattaaaacaattaatacatgatattcataaac 4444
                                                acaattggggctatgacccacagagctattttgctctttctgggatgtattcagagaaac 4384
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DB; Y27354, Y27355,
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                                                                                                   Conservative
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1362..1742
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                                                                                                                                                                                                                                                                                                                                                                                154pp; English
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                                                                                                               2.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antigens encoding
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                                                                                                 Score 74.4; DB 20
Pred. No. 4.8e-11;
0; Mismatches 208
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immunocompromise; diabetes; liver disea
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                                                                                                                                                                  1531
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RESULT 15
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                     The present invention describes a novel nucleic acid sequence which is obtainable from potato plants and carries at least a portion of an isoamylase-type debranching enzyme (DBE) gene. Constructs containing the nucleic acid sequence can be used to alter the starch properties of plants such as potato, sweet potato, maize, wheat, barley, oat, cassava, pea or rice. The starch can have increased branching and/or shorter chain length, reduced peak viscosity, higher setback viscosity or increased viscosity onset temperature. By using an antisense sequence with greater homology to the native gene, greater inhibition can be achieved. The present sequence represents a pullanase type partial length potato DBE cDNA clone from the present invention.
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Sequence 784 BP; 209 A; 161 C;

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Search completed: April 22, Job time: 2716 sec 2001, 06:56:18

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Minimum
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US-08-477-630-9
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US-08-472-293-8
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US-08-478-341-9
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ADDRESSEE: WILLIAN BRINKS HOFER GILSON & LIC
STREET: 2000 K Street, N.W., Suite 200
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,140
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Wilhiem F. Gadiano, Esq.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-41
                                                                                                                                                                                                                                                                                                                                                          Sequence 9, Application Patent No. 5721127
                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: DEWEER, PHILIPPE
APPLICANT: AMORY, ANTOINE
TITLE OF INVENTION: PULLULANASE, MICROORGANISMS WHICH
TITLE OF INVENTION: PRODUCE IT, PROCESSES FOR THE PREPARATION
TITLE OF INVENTION: PULLULANASE AND THE USES THEREOF
NUMBER OF SEQUENCES: 15
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-0625
TELEFAX: (202) 293-1850
TELEFAX: (202) 393-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 4464 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
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PROCESSES FOR THE PRE
AND THE USES THEREOF

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RESULT 3
US-08-477-630-8
US-08-477-630-8
Sequence 8, Application US/08477630
Patent NO. 5721128
GENERAL INFORMATION:
APPLICANT: DEWEER, PHILIPPE
APPLICANT: AMORY, ANTOINE
TITLE OF INVENTION: PULLULANASE, MI
TITLE OF INVENTION: PULLULANASE, MI
TITLE OF INVENTION: PULLULANASE AND
TITLE OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
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CAATICCTAAATAGTCCAGAGAACACAGTSSCCTATSAATAACTSATCATCATCATCATAAAAA
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ATTORNEY/AGENT INFORMATION:

NAME: Wilhlem F. Gadiano, Esq.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-42
REFERENCE/DOCKET NUMBER: 4121-42
RELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-6625
TELEPHONE: (202) 293-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 4464 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
US-08-477-630-8
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/477.630
FILING DATE: 07-UN-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20006
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accaacttctactcaagtaaatgttct	cacagaaagcaacaacctttaaagtctgggcacca	961	Qy	
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TELEFAX: (202) 293-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 4464 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9, Application Patent No. 5721128
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Best Local Similarity 100.0%;
Matches 2793; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,630
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Wilhlem F. Gadiano, Esq.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-42
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE WILLIAN BR
STREET: 2000 K Street
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
                                                                                                                                                                                                                  1250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: PULLULANASE, MICROORGANISMS WHICH TITLE OF INVENTION: PRODUCE IT, PROCESSES FOR THE PRETITLE OF INVENTION: PULLULANASE AND THE USES THEREOF NUMBER OF SEQUENCES: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (202) 429-0625
(202) 293-1850
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RESULT 5

Sequence 8, App
Sequence 0, App
Patent No. 5731
Pate
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ADDRESSEE: WILLIAN BRINKS HOPER GILSON & I
STREET; 2000 K Strect, N.W., Suite 200
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,293
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-44
TELECHHONE: (202) 429-0625
TELEFAX: (202) 293-1850
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                                                                                                SEQUENCE CHARACTERISTICS:
LENCTH: 4464 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
US-08-472-293-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Application Patent No. 5731174 GENERAL INFORMATION:
Query Match
Best Local :
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APPLICANT: AMORY, ANTOINE
TITLE OF INVENTION: PULLULANASE, MICROORGANISMS WHICH
TITLE OF INVENTION: PRODUCE IT, PROCESSES FOR THE PREF
TITLE OF INVENTION: PULLULANASE AND THE USES THEREOF
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3710
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CORRESPONDENCE ADDRESS:
ADDRESSE: WILLIAM BRINKS HOFER GII
STREET: 2000 K Street, N.W., Suite
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, VG
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,293
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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APPLICANT: ANORY, ANTOINE
TITLE OF INVENTION: PULLULANASE, MICROORGANISMS WHICH
TITLE OF INVENTION: PRODUCE IT, PROCESSES FOR THE PREH
TITLE OF INVENTION: PULLULANASE AND THE USES THEREOF
NUMBER OF SEQUENCES: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Wilhlem F. Gadiano, Esq. RECISTRATION NUMBER: 37,136
REPERENCE/DOCKET NUMBER: 4121-44
TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 429-0625
TELEFAX: (202) 293-1850
TELEFAX: (202) 293-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 4464 base pairs
TYPE: nucleic acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-0625
TELEPAX: (202) 293-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 4464 base pairs
TYPE: nucleic acid
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Best Local Similarity
Matches 2793; Conserv
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APPLICATION NUMBER: US/08/474,545
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Wilhlem F. Gadiano, Esq.
REGISTRATION NUMBER: 37,136
REGISTRATION NUMBER: 37,136
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NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: WILLIAN BRINK
STREET: 2000 K Street, N
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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AAA 3	# C C C C C C C C C C C C C C C C C C C	1-4 1-4 1-4	Jac 2	pat 1 GAT 3	ATC 2 ATA 2

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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic
US-08-474-545-9
                                                                                                                                                                                                                                            ADDRESSEE WILLIAN BRINKS HOFER GILSON & LICK STREET: 2000 K Street, N.W., Suite 200 CITY: Washington STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-POS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION NUMBER: US/08/474,545
FILING DATE: 07-JUN-1995
CLASSIPICATION NUMBER: US/08/474,545
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Wilhlem F. Gadiano, Esq.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4:21-43
TELECOMMUNICATION INFORMATION:
TELEPAN: (202) 429-0625
TELEPAN: (202) 239-1850
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 4464 base pairs
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Matches 2793
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: DEWEER, PHILIPPE
APPLICANT: DAWNER, ANTOINE
TITLE OF INVENTION: PULLULANASE, MICROORGANISMS WHICH
TITLE OF INVENTION: PRODUCE IT, PROCESSES FOR THE PREI
TITLE OF INVENTION: PULLULANASE AND THE USES THEREOF
NUMBER OF SEQUENCES: 15
                                1370
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             181
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Local Similarity 100.0%; Pred. No. 0;
hes 2793; Conservative 0; Mismatches
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RESULT 9
US-08-478-341-8
Sequence 6, Application US/08478341
Patent No. 5817498
Petent No. 5817498
GENERAL INFORMATION:
APPLICANT: DEWEER, PHILIPPE
APPLICANT: DEWEER, PHILIPPE
APPLICANT: MORRY, ANTOINE
TITLE OF INVENTION: PULLULANASE, MICROORGANISMS WHICH
TITLE OF INVENTION: PULLULANASE, MICROORGANISMS WHICH
TITLE OF INVENTION: PULLULANASE AND THE PREPARA:
TITLE OF INVENTION: PULLULANASE AND THE PREPARA:
CORRESPONDENCE ADDRESS: 15
CORRESPONDENCE ADDRESS: 15
CORRESPONDENCE ADDRESS: 15
COUNTRY: USA.
ZIP: 20006
CITY: Washington
STATE: D.C.
COUNTRY: USA.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
APPLICATION NUMBER: US/08/478,341
FILING DATE: 07-JUN-1995
CIASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Wilhlem F. Gaddiano, Esq.
REGISTRATION NUMBER: 37,136
REGISTRATION NUMBER: 37,136
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-45
TELEPHONE: (202) 429-0625
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                                                                      TELEPHONE: (202) 429-0625
TELEFAX: (202) 299-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 4464 base pairs
TYPE: nucleic acid
STRANDENESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic D
08-478-341-8
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                                                                                                                                                   (202) 429-0625
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2101 gcaacaggcttaactgatgcaattaagaatggcgttgaggggagtattaatgactttacc 2160

CTTTATGACAGTGCAACGGGTTCTGTAACAAAATCGTACGTA	2630 AAAGGAACAAAGGGCCCTGACAACGTAAAGACGGGGATAGATTCCTTAAAACAACTTGGG
	1381 aaaggaacaaagggccctgacaacgtaaagacggggatagattccttaaaacaacttggg
	2570 TTTTCCATTGACCCTAATTCGGGTATGAAAAATAAAGGGAAGTATTTGGCTCTTACAGAA
	1321 ttttccattgaccctaattcgggtatgaaaaataaagggaagtatttggctct
	2510 AAACATATTACGCCAAAGAATATAGAAGATGAGGTCATCTATGAAATGGATGTCCGTGAC
	1261 aaacatattacgccaaagaatatagaagatgaggtcatctatgaaatggatgtccgtgac
	2450 GGAACGAGAGGCATGATTGTGGACCTGGCTAAAACAGATCCTGCTGGCTG
	1201 ggaacgagaggcatgattgtggacctggctaaaacagatcctgctggctg
	2390 ACAGGCCAAGGCTCTACCCGAACGGCTGTTGATCCTTATGCAACTGCGATTGCACCAAAT
	1141 acaggocaaggototaccogaacggotgttgatcottatgcaactgcgattgcaccaaat
	2330 GGTGTGTGGGAAGCAACGGTTAATCAAAACCTTGAAAATTGGTATTACATGTATGAGGTA
	1081 ggtgtgtgggaagcaacggttaatcaaaaccttgaaaattggtattacatgtatgaggta
	2270 CTTTATGACAGTGCAACGGGTTCTGTAACAAAAATCGTACCTATGACGGCATCGGGCCAT
	1021 ctttatgacagtgcaacgggttctgtaacaaaaatcgtacctatgacggcatcgggccat

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RESULT 10
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                                                                                                                                                                                                                    Sequence 9, Application US/08478341 Patent No. 5817498 GENERAL INFORMATION:
     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                       APPLICANT: DEWEER, PHILIPPE
APPLICANT: AMORY, ANTOINE
TITLE OF INVENTION: PULLULANASE, MICROORGANISMS WHICH
TITLE OF INVENTION: PRODUCE IT, PROCESSES FOR THE PREI
TITLE OF INVENTION: PULLULANASE AND THE USES THEREOF
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
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                                                                                    ADDRESSEE: WILLIA STREET: 2000 K St CITY: Washington STATE: D.C. COUNTRY: U.S.A.
APPLICATION
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                                                                                                                     E: WILLIAN BRINKS HOFER GILSON 2000 K Street, N.W., Suite 200
 NUMBER:
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; TYPE: nucleic scid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic
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REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-45
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-0625
TELEPHONE: (202) 429-0625
TELEPAX: (202) 293-1850
TELEPX: 650 383-5605
INFORMATION FOR SEQ ID NO: 9:
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2793; Conservative 0; Mismatches
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LENGTH: 4464 base pairs
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Wilhlem F. Gadiano
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                                                                                                                              CAAGATGTAACCGCTGTTTTGGCAGGTACCTTCCAACATATTTTTGGAGGTTCCGATTGG
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                         CCGAGTTACCCATCTGACAACATTAAATTTAACAGTCCCTGCCGGCGGTGCACACGTCACT
                                                                             GGAGATCTTCCTGAAGGAAACTACCAATATAAAGTGGCTTTAAATGATAGCTGGAATAAT
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1740 2989	1681 totgachtogataaaattgtacoagaatattattacogtacgatgatooaggtaattata 	B 8
1680 2929	1621 cgtgaacacattggggttaacatggatgttgtctataatcatacctttgccacgcaaatc	Οy
1620 2869	1 acaaatgcgaatggtaatgctcgtataaaagagtttaaggaaatggttctttcactccat 	B 8
1560 2809	1501 acccaagataattggggttatgaccctcgcaactatgatgttcctgaagggcagtatgct 	g ç
1500 2749	1441 attactcatgttcagcttatgcctgttttcgcatctaacagtgtcgatgaaactgatcca 	D _b
1440 2689	1381 aaaggaacaaagggcctgacaacgtaaagacggggatagattccttaaaacaacttggg 	рb
1380 2629	1321 ttttccattgaccctaattcgggtatgaaaaataaagggaagtatttggctcttacagaa 	Оy
1320 2569	1261 aaacatattacgccaaagaatatagaagatgaggtcatctatgaaatggatgtccgtgac 	Db Qy
1260 2509	1201 ggaacgagaggcatgattgttggacctggctaaaacagatcctgctggctg	pb qq
1200	1141 acaggccaaggctctacccgaacggctgttgatccttatgcaactgcgattgcaccaaat	D _Q
1140 2389	1081 99t9t9t999aagcaacg9ttaatcaaaaccttgaaaatttg9tattacat9tattgag9ta 	Qу
1080 2329	1021 ofttatgacagtgcaacgggttctgtaacaaaaatcgtacctatgacggcatcgggccat	Db Oy
1020 2269	961 acacagaaagcaacaacctttaaagtctgggcaccaacttctactcaagtaaatgttctt 	Ωy
960 2209	901 ogtaatgtgottaattcatcacagtactactattcaggagatgatcttgggaatacctat 	Оу
900 2149	841 gatgtgagccatactctgtccattcaaacagatggctatcaggcaaagcaggtgatacct 	gb Qy
840 2089	781 ttacaagtagaaagcggggttaaaaccggatctcgtgacggttactctaggggaagatcca	р _р
2029		đđ

	2761 gtaagcccagaccacggtaaaaagtaatagaaaa 2794	P 6
8	95	Db
3949 2760	TGCCGAGCGGGAAATGGGCAATCAATGCTACGAGCGGTAAGGTAGGAGAATCCACCCT qtcaaqcaqaaqqaaattqtccaaqtaacaaqtatatatctattattattattatcatcatcaaca	O 5
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- 8	830 GACAAATGGGGAAATATCATTGTTGTTATAACCCAAATAAAACTGTAGCAACCATCAAT	· B
2640	85	Qy
3829	AATTCCTAAATAGTCCAGAGAACACAGTGGCCTATGAATTAACTGATCATGTTAATAAA	DЬ
2580		40
3769	3710 CTTCGTCTTGATCACCCAGCCTTCCGCATGACGACAGCTAATGAAATCAATAGCCACCTC	В
2520	461 ottogtottgatcacccagcottccgcatgacgacggctaatgaaatcaatagccacctc	Qy
3709	TGGAGCAGGAAAGCTCAATATCCAGATGTTTTCAACTATTATAGCGGGCTAATCCAC	망
2460	attggagcaggaaagctcaatatccagatgttttcaactattataqcgggctaatccac	Qy
3649	TCGTANAAAAGGCGGCAACGACAATAGTTATAATGCAGGCGATGCGGTCAATGAGTTT	₽
2400	ttcgtanaaaaggcggcaacgacaatagttataatgcaggcgatgcggtcaatgagttt	Qy
3589	3530 GCACAAGCAGTTGTTATGACCTCACAAGGCGTTCCATTCATGCAAGGCGGGGAAGAAGTG	DЬ
2340	cacaagcagttgttatgacctcacaaggcgttccattcatgcaaggcggggaagaaatg	Qy
3529	3470 AAAATAGCCCTAAGCAATCCTAATGATTCCGAAGCGGATCGGATTAAAATGGATGAACTC	Db
2280	atagccctaagcaatcctaatgattccgaagcggatcggattaaaatggatgaact	Qy
3469	3410 TCTTCACCAGGTGAGACAATTAACTATGTCACAAGTCATGATAACTACACCCTTTGGGAC	DЬ
2220	cttcaccaggtgagacaattaactatgtcacaagtcatgataactacaccctttggga	Qy
3409	3350 GCAACAGGCTTAACTGATGCAATTAAGAATGGCGTTGAGGGGAGTATTAATGACCTTTACC	Дb
2160	1 gcaacaggcttaactgatgcaattaagaatggcgtttgaggggagtattaatgactttacc	Qy
3349	3290 TTACGAAACGCGTTGGACGGCAATGTCTTTGATTCTTCCGCTCAAGGTTTTGCGACAGGT	ДЬ
2100	Lacgaaacgcgttggacggcaatgtctttgattcttccgctcaaggtttttgcgacaggt	Qy
3289	3230 GATCAGCTTCTGACAAAAGGAGCTCAAAAAGGCATGGGAGTAGCGGTGTTTAATGACAAT	d d
2040	atcagcttctgacaaaaggagctcaaaaaggcatgggagtagcggtgtttaatgacaat	Qy
3229	3170 AATCCAGGAATTGCACTTTACGGTGAGCCATGGACGGGTGGAACCTCTGCCACTGCCAGAT	망
1980	atccaggaattgcactttacggtgagccatggacgggtggaacctctgcactgccaga	Qy
3169	3110 TTAATGGCGCTGGTTGGAAAAGACACGATGTCCAAAGCTGCCTCGGAGCTTCATGCTATT	망
1920	taatggcgctgcttggaaaagacacgatgtccaaagctgcctcggagcttcatgctat	Qy
3109	3050 ATTATTGATTCCCTTAAGTATTGGGTCAATGAGTATCATATTGACGGCTTCCGTTTTGAC	Db

RESULT 11
US-08-996-733-8
; Sequence 8, Application US/08996733
; Patent No. 6074854
; GENERAL INFORMATION:
; APPLICANT: DEWEER, PHILIPPE

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4010 GTAAGCCCAGACCACGGTAAAAAGTAATAGAAAA 4043

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; MOLECULE TYPE: genomic DNA
US-08-996-733-8
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOETWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,733
FILING DATE: 23-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,293
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/174,893
FILING DATE: 08-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/174,893
FILING DATE: 28-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/174,893
                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 99.7%; Score 2786.4; Best Local Similarity 100.0%; Pred. No. 0; Matches 2793; Conservative 0; Mismatches
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NFORMATION FOR SEQ ID NO: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: POETR INFORMATION:

NAME: POETR INFORMATION:

NAME: OEbra J. Glaister, Esq.

REGISTRATION NUMBER: 33,888

REFERENCE/DOCKET NUMBER: GC446C1-US

TELEPHONE: (650) 846-7620

TELEPHONE: (650) 846-7620
                                                                                                                                         APPLICATION NUMBER: BE 09301278
FILING DATE: 19-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: BE 09300744
FILING DATE: 15-JUL-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                             1250 GATGGGAACACGACAACGATCATTGTCCACTATTTTTGCCCTGGTGATTATCAACCT 1309
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                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 4464 base pair
                                                                          181 attatogttogcactcaagattyggaccaaagatgtgagcgctgaccgctacatagattta 240
  241 agcaaaggaaatgaggtgtggcttgtagaaggaaacagccaaattttttataatgaaaaa 300
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CITY: Palo Alto,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.
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                                                  ATTATCGTTCGCACTCAAGATTGGACCAAAGATGTGAGCGCTGACCGCTACATAGATTTA 1489
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925 Page Mill Road
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1380	ttttccattgaccctaattcgggtatgaaaaataaagggaagtatttggctcttacagaa	w	Qy
2569	AAACATATTACGCCAAAGAATATAGAAGATGAGGTCATCTATGAAATGGATGTCCGTGAC	2510	da
1320	aacatattacgccaaagaatatagaagatgaggtcatctatgaaatggatgtccgtga	N	Qy
50		2450	Db
26	qaacqaaaqqcatqattqtqqacctqqctaaaacaqatcctqctqqctq	20	0 _V
2449	acayycaayyccaayyccaayyccaayycgaagygaagaagaagaagaagaagaagaagaagaagaaga	2390	B 3
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2389	geTGTGTGGGAAGCAACGGTTAATCAAAACCTTGAAAATTTGGTATTACATGTATGAGGTA	2330	B 7
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2269	a cacagaaay cacaactee taaay too yyy caccaactee too aag taaay too too aag taa yoo aa yoo aa yoo aa yoo aa yoo a	2210	B 4
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2089	TTACAAGTAGAAAGCGGGGTTAAAAACGGATCTCGTGACGGTTACTCTAGGGGAAGATCCA	2030	фa
840	tacaagtagaaagcggggttaaaacggatctcgtgacggttactctaggggaagatcca	781	Qy
2029	TTTTCGTATATTCCGTCCACTCATGCAGTCTATGACACAATTAATAATCCTAATGCGGAT	1970	Дb
780	tttcgtatattccgtccactcatgcagtctatgacacaattaataatcctaatgcgga	721	Qy
1969	CCGAGTTACCCATCTGACAACATTAATTTAACAGTCCCTGCCGGCGGTGCACACGTCACT	1910	Db
720	cyagitacccatcigacaacattaatitaacagicccigccggcggigcacacgicac	661	Qy
1909	GGAGATCTTCCTGAAGGAAACTACCAATATAAAGTGGCTTTAAATGATAGCTGGAATAAT	1850	Дb
660	gagatottootgaaggaaactaocaatataaagtggotttaaatgatagctggaataa		Qy
1849	GCACCTGATAATCACAGTACTTTATTAAAAAAAGGTGACTAACAATCTCTATCAATTCTCA	1790	ДĎ
600	cacctgataatcacagtactttattaaaaaaggtgactaacaatctctatcaattctc	541	Qy
1789	CAAGATGTAACCGCTGTTTTGGCAGGTACCTTCCAACATATTTTTTGGAGGTTCCGATTGG	1730	ДĎ
540	aagatgtaaccgctgttttggcaggtaccttccaacatattttttggaggttccgattg	481	Оу
1729	CATGACGACAGCAAATAAGGATATTCCAGTGACATCTGTGAAGGATGCAAGTCTTGGT	1670	Db
480	atgacgacacagcaaataaggatattccagtgacatctgtgaaggatgcaagtcttgg		Qy
1669	GTGCTGGTTAAACTTAGCCAGCCGTTAACTCTTGGGGAAGGNNNAAGCGGCTTTACGGTT	1610	Db
420	tyctyyttaaacttayccayccyttaactcttygygaaggnnnaagcygctttacyc		Оy
1609	GATGCTGAGGATGCAGCTAAACCCGCTGTAAGCAACGCTTATTTAGATGCTTCAAACCAG		DЬ
	algotyaggatgcagotaaaccogotgtaagcaacgottatttagatgottcaaacc		Qy
1549	AGCAAAGGAAATGAGGTGTGGCTTGTAGAAGGAAACAGCCAAATTTTTTTATAATGAAAAA	1490	Db

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                            gcacaagcagttgttatgacctcacaaggcgttccattcatgcaaggcggggaagaaatg
                                                                                           aaaatagccctaagcaatcctaatgattccgaagcggatcggattaaaatggatgaactc
AAAGGAACAAAGGCCCCTGACAACGTAAAGACGGGGGATAGATTCCTTAAAACAACTTGGG
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US-08-996-733-9; Sequence 9, Ap; Patent No. 607; GENERAL INFOR
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APPLICATION UNBER: US/08/996,733
FILLING DATE: 23-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,293
FILLING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 08/174,893
FILLING DATE: 28-DEC-1993
PRIOR APPLICATION UNBER: BE 09301278
FILLING DATE: 19-NOV-1993
PRIOR APPLICATION UNBER: BE 09300744
FILLING DATE: 19-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: BE 09300744
FILLING DATE: 15-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: BE 09201156
FILLING DATE: 28-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: DEBTA J. GLAISTER: ESG.
REGISTRATION NUMBER: GC446C1-US
TELEPHONE: (650) B46-7620
                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Genencor Internatic STREET: 925 Page Mill Road CITY: Palo Alto, STATE: CA COUNTRY: U.S.A. COUNTRY: U.S.A. ZIP: 94304 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DC SOFTWARE: Patentin Release #1. CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: DEWEER, PHILIPPE
APPLICANT: AMORY, ANTOINE
TITLE OF INVENTION: PULLULANASE,
TITLE OF INVENTION: PRODUCE IT, P
TITLE OF INVENTION: PULLULANASE A
NUMBER OF SEQUENCES: 15
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925 Page Mill Road
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INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 4464 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
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Local Similarity 100.0%;
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                     ttttcgtatattccgtccactcatgcagtctatgacacaattaataatcctaatgcggat
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US-08-474-140-10
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                                         APPLICANT: DEWEER, PHILIPPE
APPLICANT: AMORY, ANTOINE
TITLE OF INVENTION: PULLULANASE, MICROORGANISMS WHICH
TITLE OF INVENTION: PRODUCE IT, PROCESSES FOR THE PREF
TITLE OF INVENTION: PULLULANASE AND THE USES THEREOF
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
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ADDRESSEE: WILLIAN BRINKS HOFER GILSON STREET: 2000 K Street, N.W., Suite 200 CITY: Washington
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REFERENCE/DOCKET NUMBER: 4121-41
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-0625
TELEPAX: (202) 293-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 2784 base pairs
TYPE: nucleic scid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
US-08-474-140-10
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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COUNTRY:
ZIP: 200
COMPUTER RE
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NAME: Wilhlem F. Gadiano, E.
REGISTRATION NUMBER: 37,136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
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                                        CAAGATGTAACCGCTGTTTTGGCAGGTACCTTCCAACATATTTTTTGGAGGTTCCGATTGG
                                                  caagatgtaaccgctgttttggcaggtaccttccaacatatttttggaggttccgattgg
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STREET: 2000 K Street, N.W., Suite 2
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC LOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION UNMEER: US/08/477,630
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/ACFNT INCOMMATION:
                                                                                                                                                                                                                                                                                      MOLECULE TYPE: -08-477-630-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 5721128 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (202) 293-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
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APPLICANT: AMORY, ANYOINE
TITLE OF INVENTION: PULLUI
TITLE OF INVENTION: PRODUC
TITLE OF INVENTION: PULLUI
                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Wilhlem F. Gadiano, Esq.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-42
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                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: sing
TOPOLOGY: linear
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Local Similarity
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(202) 293-1850
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linear
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MEDIUM TYPE: FIDPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-POS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/472,293
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WILHOM F. Gadlano, Esq.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-44
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-0625
TELEFAX: (202) 293-1850
INFORMATION FOR SEQ ID NO: 10:
CENTIFER SEQ ID NO: 10:
                                                                                             TOPOLOGY: 1:
; MOLECULE TYPE:
US-08-472-293-10
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US-08-472-293-10
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Matches 2783;
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Patent No. 5
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APPLICANT: DEWEER
APPLICANT: AMORY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: WILLIAN BRI
STREET: 2000 K Street,
STATE: D.C.
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 2784 base pairs
TYPE: nucleic acid
STRANDENESS: single
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APPLICANT: AMORY, ANTOINE
TITLE OF INVENTION: PULLULANASE, MICROORGANISMS WHICH
TITLE OF INVENTION: PRODUCE IT, PROCESSES FOR THE PREPARATION OF
TITLE OF INVENTION: PULLULANASE AND THE USES THEREOF
NUMBER OF SEQUENCES: 15
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b; Score 2776.4;
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Search completed: April 22, 2001, 07:58:35 Job time: 5969 sec

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GenCore version (c) 1993 - 2000

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Search time 44.44 Seconds

Scoring table:

IDENTITY_NUC Gapop 10.0 ,

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Title: Perfect score:

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GENERAL INFORMATION:
APPLICANT: Miller, Brian S.
APPLICANT: Shetty, Jayarama K.
TITLE OF INVENTION: Modified Forms of Pullulanase
FILE REFERENCE: GC396-2
CURRENT APPLICATION NUMBER: US/09/262,126C
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 9
SOFTMARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 2794
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Result No.

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APPLICANT: Smith, A.
APPLICANT: Bustos GI
APPLICANT: Martin, G
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Matches 164; Conserv
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SEQ ID NO 2
LENGTH: 2706
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CURRENT FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: PCT/GB98/02280
PRIOR FILING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: GB 9716185.5
PRIOR FILING DATE: 1997-07-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Martin, Catherine R
APPLICANT: Plant Bioscience Limited
TITLE OF INVENTION: Starch Debranching Enzymes
FILE REFERENCE: 97.118
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Pred. No. 3.6e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches 132;
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                                                       APPLICANT: Martin, Catherine R
APPLICANT: Plant Bioscience Limited
TITLE OF INVENTION: Starch Debranching Enzym
FILE REFERENCE: 97.118
CURRENT APPLICATION NUMBER: US/09/463,238
CURRENT FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: PCT/GB98/02280
PRIOR FILING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: GB 9716185.5
PRIOR APPLICATION NUMBER: GB 9716185.5
PRIOR FILING DATE: 1997-07-31
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LENGTH: 2806
TYPE: DNA
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Best Local Similarity
Matches 89; Conserv
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CURRENT FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: PCT/GB98/02280
PRIOR FILING DATE: 1998-07-30
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NUMBER OF SEQ ID NOS: 30 SOFTWARE: PatentIn Ver. 3EQ ID NO 1
                                                                                                                                                                                                                                                                         APPLICANT: Smith, Alison M
APPLICANT: Bustos Guillen, Regla
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Bustos Guillen, Regla
Martin, Catherine R
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Pred. No. 0.0034;
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; TYPE: DNA
; ORGANISM: Solanum tuberosum
US-09-463-238-1
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; OTHER INFORMATION: n - a or g or c or
US-09-463-238-10
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Sequence 3, Application US/09463238
GENERAL INFORMATION:
APPLICANT: Edwards, Elizabeth A
APPLICANT: Smitch, Alison M
APPLICANT: Bustos Guillen, Regla
APPLICANT: Hartin, Catherine R
APPLICANT: Plant Bioscience Limited
TITLE OF INVENTION: Starch Debranching Enzymes
FILE REFERENCE: 97.118
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NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 2843
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Best Local Similarity
Matches 67; Conserv
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Best Local Similarity
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APPLICANT: Smith, Alison M
APPLICANT: Bustos Guillen, Regla
APPLICANT: Bustos Guillen, Regla
APPLICANT: Martin, Catherine R
APPLICANT: Plant Bloscience Limited
TITLE OF INVENTION: Starch Debranching Enzymes
FILE REFERENCE: 97.118
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CURRENT FILING DATE: 2000-01-21
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NAME/KEY: mlsc_feature
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Pred. No. 0.16;
0; Mismatches 48;
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CURRENT APPLICATION NUMBER: US/09/463,238
COURRENT FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: PCT/GB98/02280
PRIOR FILING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: GB 9716185.5
PRIOR FILING DATE: 1997-07-31
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
SEO ID NO 3
LENGTH: 2634
TYPE: DNA
ORGANISM: Solanum tuberosum
US-09-463-238-3
RESULT 8
US-60-248-505-164
; Sequence 164, Application US/60248505
; GENERAL INFORMATION:
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; LCGATION: (1)...(264546)
; OTHER INFORMATION: n = A
US-60-248-505-202
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LENGTH: 264546
TYPE: DNA
ORGANISM: human
FEATURE:
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APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: cl000918
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Best Local Similarity
Matches 53; Conserv
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Best Local Similarity 51.6%;
Matches 82; Conservative
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SOFTWARE: FASTSEQ for Windows Version 4.0
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CURRENT FILING DATE: 2000-11-15
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                                                                                                                                         34150 aaaactaataagtgagtttatcagggttgcagacaagat 34188
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; NAME/KEY: misc_feature
; LOCATION: (1)...(133937)
; OTHER INFORMATION: n - A,T,C or
US-60-248-822-8
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; ORGANISM: human
US-60-248-505-164
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                                                                                                                                                 Db 120075 ttctggaggttaggaagcttagaaggtgaatggttatcaacttttacaatagttttaaca
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TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN
TITLE OF INVENTION: RECEPPORS, NUCLEIC ACTI
TITLE OF INVENTION: PROTEINS, AND USES THEF
FILE REFERENCE: C1000918
CURRENT APPLICATION NUMBER: US/60/248,505
CURRENT FILING DATE: 2000-11-15
NUMBER OF SEQ ID NOS: 1998
                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 68; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 133937
TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/60248822
GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
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SEQ ID NO 164
LENGTH: 91051
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Best Local Similarity 49.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: CL000960
CURRENT APPLICATION NUMBER: US/60/248,822
CURRENT FILING DATE: 2000-11-16
NUMBER OF SEO ID NOS: 30
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120195
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                                                                                             1602 aatggttctttcactccatcgtgaacacattggggttaacatggatgttgtctataatca 1661
                                                                                                                                                                       1499 caacccaagataattggggttatgaccctcgcaactatgatgttcctgaagggcagtat 1557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1379 aaaaaggaacaaagggccctgacaacgtaaagacgggggatagattccttaaaacaacttg 1438
                                    1662 tac 1664
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                                                                        aagagtttatttatcaaaattacacacggcaaaaaatacaatgctatttcattttacaca
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120197
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TROTADERS NUCLEIC ACID MOLECULES ENCODING HUMAN GECR
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Pred. No.
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28;
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                                                                                                                                                                                                                                                                  Length 133937;
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NAME/REY: misc_feature

LOCATION: (1)...(2794)

OTHER INFORMATION: n -

US-09-262-126C-1
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US-09-262-126C-1/c
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NAME/KEY: misc_feature; LOCATION: (1)...(22788); OTHER INFORMATION: n = US-60-248-505-127
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GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: C1000918
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CURRENT FILING DATE: 2000-11-15
NUMBER OF SEQ ID NOS: 1998
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 127
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Shetty, Jayarama K.
TITLE OF INVENTION: Modified Forms of Pullulanase
FILE REFERENCE: GC396-2
CURRENT APPLICATION NUMBER: US/09/262,126C
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ. ID NOS: 9
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                                                                                                    ORGANISM: human
                                                                                                                            TYPE: DNA
                                                                                     FEATURE:
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                                                                                                                                                LENGTH: 22788
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            atttgccgagcgggaaatgggcaatcaa 2666
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                     A,T,C
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SEQUENCE 354, Application US/60248505
GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID
TITLE OF INVENTION: PROTEINS, AND USES THER
FILE REFERENCE: c1000918
CURRENT APPLICATION NUMBER: US/60/248,505
CURRENT FILING DATE: 2000-11-15
NUMBER OF SEQ ID NOS: 1998
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 354
LENGTH: 55248
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TITLE OF INVENTION: ISOLARIED HUMAN G-PROTEIN
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID
TITLE OF INVENTION: PROTEINS, AND USES THER
FILE REFERENCE: C1000918
CURRENT APPLICATION NUMBER: US/60/248,505
CURRENT FILING DATE: 2000-11-15
NUMBER OF SEQ ID NOS: 1998
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 611
LENGTH: 30167
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; ORGANISM: human
US-60-248-505-611
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Best Local Similarity
Matches 87; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 1.2%;
Bost Local Similarity 60.0%;
Matches 57; Conservative
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ORGANISM: human
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NAME/KEY: misc_feature
LOCATION: (1)...(55248)
OTHER INFORMATION: n =
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15721 GTTAGCAGTGGGCTTGTGATTTATGGCTTTATGATTCTGTACCTAATTTGTTTAGAATTT 15662
                                                             FEATURE:
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                     (55248)
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RECEPTORS, NUCLEIC ACID MOLECULES ENCODING
PROTEINS, AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.28;
     A, T, C
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Pred. No. 20;
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Pred. No. 17;
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; LENGTH: 61635
; TYPE: DNA
; ORGANISM: human
US-60-248-505-254
; FEATURE:

NAME/KEY: misc_feature

: LOCATION: (1)...(150471)

: OTHER INFORMATION: n = A

US-60-248-505-148
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Best Local Sim
Matches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 254, Application US/60248505
GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULE
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: C1000918
CURRENT APPLICATION NUMBER: US/60/248,505
CURRENT FILING DATE: 2000-11-15
                                                                                                                                                                                                                                              Sequence 148, Application US/60248505
GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: C100018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 60.0
Matches 57; Conservative
                                                                                                                                                     SOFTWARE: FastSEQ
SEQ ID NO 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 254
                                                                                         LENGTH: 150471
TYPE: DNA
ORGANISM: human
                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/60/248,505 CURRENT FILING DATE: 2000-11-15
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SOFTWARE: FastSEQ for
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Search completed: April 22, 2001, 09:12:11 Job time: 8392 sec

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Copyright (c) 1993 - 2000
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em_estr01:

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gb_est48:*
gb_est49:*
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Match
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532
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893
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AW727770
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BE493792
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AW697292
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9b_est90:*
9b_est99:*
9b_est100:*
9b_est100:*
9b_est100:*
9b_cst102:*
9b_cst103:*
9b_cst104:*

gb_est68: gb_est70:

gb_est106:

gb_est88:

gb_est86:

9b_est76:*
9b_est77:*
9b_est778:*
9b_est89:*
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9b_est82:*
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gb_est64:*
gb_est65:*
gb_est66:*
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gb_est60:*
gb_est61:*
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gb_est56:* gb_est58:* gb_est58:*

9b_est71: *
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9b_est

AW727770 GA_E0002
AZ67343 ENTIK90TR
BE433792 WHE1275_E
AL106431 Drosophil
AQ100007 HS_3054_B
BG227648 Kq13±10.y
A1737641 605036610
BE444461 WHE1111_H
AW657292 NF117004S
BF587295 FM1_34_F0
AW730507 GA_E0002
AZ532406 ENTBY35TF
AZ688071 ENTJF17TF
AW832588 SM14507.y
AZ549196 ENTGY38TF
AW034518 EST278134

Description

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BASE COUNT
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                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clemson University
100 Jordan Hall, Cl
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                          AW727770 874 bp mRNA EST 16:NOV-2000 GA_EA0028A17 Gossypium arboreum 7-10 dpa fiber library Gossypium arboreum cDNA clone GA_Ea0028A17, mRNA sequence.

AW727770
                                                                                                                                                                                                                                   Unpublished (2000)
Contact: Wing RA
                                                                                                                                                                                                                                                        Wing.R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J., Henry,D., Wood,T.C., Leslie,A. and Wilkins,T.A.
An integrated analysis of the genetics, development, and evolution of the cotton fiber
                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
                                                                                                                                                                                                                                                                                                                                              Gossypium arboreum.
Gossypium arboreum
                                                                                                                                                                                                                                                                                                                                                                     AW727770.1 GI:7625331 EST.
                                                                                                                                                       Email: rwing@clemson.edu
High quality sequence st
                                                                                                                                                                                                                        Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                Malvales;
                                                                                                                                                                                                                                                                                                 (bases 1 to 874)
            ы
          /note-*Vector: pBK-CMV; Site_1: EcoRI; Site_2: xhoI*
148 c 225 g 261 t 2 others
                                                     /db_xref="taxon:29729"
/clone="GA_Ea0028A17"
/clone_lb-"Gossyplum arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-10
                                                                                                                                         ity sequence stop: Location/Qualifiers
                                                                                                            /organism="Gossypium arboreum"
/strain="AKA"
                                 /lab_host="E. coli"
                                                                                                  /cultivar-"8400"
                                                                                                                                                                                                                                                                                                               Malvaceae; Gossypium.
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AQ935730
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CNS03FGA
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CNS0163T
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AQ280563 CITPSI-E1-
AQ280703 CITBSI-E1-
AQ280703 CITBSI-E1-
AQ935730 CPC25620A
AZ676090 ENTLQ90TR
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AW506191 GE1528 GL
BE870915 601448867
BE681758 179528 MA
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AI653243 wb44c06.x
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BF373589
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Seq primer: M13-Reverse
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Class: shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: bjloftus@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Entamoebidae;
1 (bases 1 to 974)
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/clone_lib="Entamoeba histolytica Sheared DNA"
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/note="Vector: pHOSI; Site_1: Bst I; Co
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Anderson,O.D., Butler,E., Chao,S., Choi,D.W., Close,T.J., Fentol,R.D., Gustafson,J.P., Han,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Ross,K., Seaton,C.L. and Tong,J.C.
The structure and function of the expressed portion of the whea genomes - Anther cONA ilbrary from rye Unpublished (2000)
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BE493792
BE493792.1 GI:9660385
                                                                                         Email: oandersn@pw.usda.gov
Sequence have been trimmed to reme
quality sequence with phred score
                                                                                                                                                                       Contact: Olin Anderson
US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
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/organism="Secale cereale'
/cultivar="Blanco"
                                                       Location/Qualifiers
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                                                                                                                                                                                                     Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster genome survey sequence SP6 end of BAC BACN15C22 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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Site_1: EcoRI; Site_2: XhoI; Plants were grown in the
greenhouse. Anthers were harvested and pooled from early
meiosis to late meiosis. The tissue, total RNA, and
poly(A) RNA were prepared (Butler, Ross and Gustafson) at
University of Missouri, Columbia. A cDNA library was
made, and the cDNA clones were in vivo excised to give
pBluescript phagemids in the TJ Close lab (Choi, Close,
Fenton) at the University of California, Riverside.
Plasmid DNA preparations and DNA sequencing were performed
in the OD Anderson lab (all other authors)."
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/clone="WHE1275_E05_109"
/clone_lib="Secale cereale anther cDNA library"
/clone_lib="DrosBAC"
/clone="BACN15C22"
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/dev_stage="Adult plant before anthesis"
/lab_host="E. coli SOLK"
                                                   /db_xref="taxon:7227"
                                                                            /organism-"Drosophila
/plasmid-"pBeloBAC11"
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Pred. No. 0.096;
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                                       Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org the BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
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   /organism="Drosophila
/db_xref="taxon:7227"
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Pred. No. 0.22;
09; Mismatches
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99380589
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Contact: Mahairas
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HS_3054_B1_F07_MF CIT Approved Human Genomic Sperm Library D
sapiens genomic clone Plate-3054 Col-13 Row-L, DNA sequence.
AQ100007
AQ100007.1 GI:3471036
                                       Sequence-tagged connectors: scanning the human genome Proc. Natl. Acad. Sci. U. S.
                                                                                                                             Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S.,
                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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/clone="BACR08K10"
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a 64 c 131 g
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Local Similarity 50.2%;
hes 106; Conservative
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Fax: (206) 616-3867
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3054 row: L column: 13
Class: BAC ends
High quality sequence stop: 373.
Location/Qualifiers
                                                                                                                                                        McCarter, J., Clifton, S., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylic, T., Undorwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
The Washington Univ. Nematode EST Project, 1999
Unpublished (1999)
Contact; McCarter JP
                                                                                                                                                                                                                                                                                                                                                                                                                                      BG227648 · 558 bp mRNA EST 08-FEB-2001 Kq13e10.y1 TBN95TM-SSR Strongyloides stercoralis cDNA 5' similar WP:T10F2.1 CE02040 GLYCYL-TRNA SYNTHETASE ;, mRNA sequence. BG227648 G1:12715282
                                     Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                              The Washington Univ. Nematode EST Project, 1999 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                     Strongyloides stercoralis
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Panagrolaimoidea; Strongyloididae; Strongyloides.
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University of Washington
                                                                                                                                                                                                                                                                                                                   (bases 1 to 558)
                  library was constructed by Dr.
  NIH (tnutman@nih.gov).
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E-Coli DH10B"
1 36 c 67 g 120 t
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/sex="male"
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/db_xref="taxon:9606"
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Pred. No. 0.31;
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. Thomas Nutman Sequencing by:
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and colleagues Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                al Similarity
125; Conserv
Stanford University
855 California Ave, Palo
Tel: 650 723 2227
Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AI737641 644 bp mRNA EST 02-FEB-20 605036B10.x2 605 - Endosperm cDNA library from Schmidt lab
                                                                                                                                               Unpublished (1999)
Contact: Walbot V
                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae
                                                                                                                                                                                                                                                                                                                                                                                                         Zea mays
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                                                                                                                     Department of Biological Sciences
                                                                                                                                                                                                                            Walbot, V.
Maize ESTs from various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AI737641.1 GI:5069676
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/note="Vector: Lambda Uni-ZAP XR (Stratagene); Site_1:
ECORI; Site_2: xhol; mRNA was purified from 2 x 10E3
rhabditiform larvae which had been isolated from gerbils
experimentally infected with larvae originally isolated
from experimentally infected dogs. cDNA was constructed
and, using adaptors, was cloned unidirectionally into the
vector from the ECORI site to the Xhol site. The library
has an unamplified titer of 1 x 10E5 pft/ml and an
amplified, undiluted titer of 9 x 10E11 pfu/ml. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 average insert size of the unamplified library is 675 bp (range, 100-1700)."
71 c 100 g 182 t
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/strain="Rhabdittiform larvae obtained from
/db_xref="taxon:6248"
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                                                             Alto, CA 94304, USA
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Triticum aestivum
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Mamnollophyta; Lillopsida; Poales; Poaceae; Pooldeae; Triticeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BE444461 612 bp mRNA EST 25-JUL-2000 WHE1111_H10_P19ZS Wheat etiolated seedling root normalized cDNA library Triticum aestivum cDNA clone WHE1111_H10_P19, mRNA
                                                                                                                              quality sequence with phred score less Seq primer: Stratagene SK primer.
                                                                                                                                                                                                                         800 Buchanan Street,
Tel: 5105595773
                                                                                                                                                                                                                                       genomes - Normalized root cDNA library Unpublished (2000)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research West Area, Western Regional Research Center 800 Buchanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                                                  Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., H., P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T., Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.

The structure and function of the expressed portion of the wh
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                                                                                                                                                                    Sequence have been trimmed to remove vector
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                                                                                                                                                                                   Email: oandersn@pw.usda.gov
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605036 row: B col
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Site_2: XhoI; Kernel endosperm cDNA library from Schmidt
/organism-"Triticum aestivum"
/culiivar-"Chinese Spring"
/db_xref-"taxon:4565"
/clone-"WHED111_H10_P19"
/clone_lib-"Wheat etiolated s
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/clone_lib="605 - Endosperm cDNA library from Schmidt lab"
/tissue_type="nucellar, embryo, and endosperm"
/dev_stage="10-14 days post-pollination"
/lab_host="DH5(alpha)"
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/cultivar="Ohio43"
                                                                                                            ocation/Qualifiers
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Pred. No. 0.75
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                                                                                                                                                                                                                                                                             Service, Pacific
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                                                                                                                                                                                                                                 AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGTGACGAGATACTAAGATCTAAGTCCATTGATCGAGATTCATACAACTCTGGTGATTGG
                                                                                                                                                                                               Medicago truncatula
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papilionoideae; Medicago.

1 (bases 1 to 365)
He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell
He,X.-Z., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Dixon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AW697292 365 bp mkNA
MF117C04ST1F1033 Developing stem Medicago
NF117C04ST 5', mkNA sequence.
                                                                         Unpublished (2000)
On Apr, 14, 2000 th
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  Plant Biology Division
The Samuel Roberts Nob
                                               Contact: Dixon RA
                                                                                                                        Expressed Sequence Tags from the Medicago truncatula stem library
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  Samuel Roberts Noble
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/lab_host="E. coli DH10B"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid
/note="Vector: Lambda Uni-ZAP XR, excised phagemid
pBluescript SK; Site_1: EcoRI; Site_2: xhoI; Seeds were
surface-sterilized, germinated and grown aseptically in
the dark at room temperature on filter paper with water,
nystatin and cefotaxime in covered crystallization
dishes Roots were harvested. The tissue, total RNA, and
poly(A) RNA were prepared, a cDNA library was made in the
TJ Close lab (Choi, Close, Fenton) at the University of
California, Riverside. The cDNA clones were in vivo
excised to give pBluescript phagemids before
normalization was carried out. The mass excision of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     normalization was carried out. The mass excision of phagemid library and normalization were done in HT Nguyei lab by D. Zhang at Texas Tech University. Normalization protocol used was that of Soares. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type-"Root"
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                                                                      this sequence version
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Pred. No. 1.
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Foundation
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                                                                         replaced gi:7572054
                                                                                                                                                     Roberts
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Best Local Similarity
Matches 62; Conserv
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                                                                                                                                                                                                                                                                                                                             Unpublished (2000)
Contact: Cordonniter-Pratt MM
Department of Botany
The University of Georgia
Plant Sciences Building, Rm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sorghum propinquum
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae
                                                                                                                                                                                                                                  Email: mmpratt@uga.cdu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    propinguum cDNA, mRNA sequence BF587295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BF587295 532 bp mRNA FM1_34_F08.b1_A003 Floral-Induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: radixon@noble.org
Insert Length: 778 Std Error: 0.(
Plate: 117 row: C column: 04
Seq primer: TCACACAGGAAACAGCTATGAC.
                                                                                                                                                                                              Seq primer: JEN REV
                                                                                                                                                                                                                                                                                                                                                                                                                                An EST database from Sorghum: floral-induced meristems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cordonnier-Pratt, M.-M., Gingle, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sorghum propinquum.
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706 542 1805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Modicago truncatula"
/db_xref="taxon:3880"
/clone="well7c04ST"
/clone_lib="Developing stem"
/tissue_type="stem"
/dev_stage="Pooled developmental"
/note="Vector: Lambda Zap; Contains a mixture of internodal stem segments"
a 65 c 95 g 110 t
              /organism="Sorghum propinguum"
/db_xref="taxon:132711"
/clome_iib="Floral-Induced Meristem 1 (FM1)"
/note="Organ: Floral-induced meristems; Vector:
pBluescript II from Lambda Zap II; Site_1: Xhoi;
EcoRI; mature plants were placed in a growth chamber
                                                                                                                                     Location/Qualifiers
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Pred. No. 2.
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Best Local Similarity 49.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1402 aacgtaaagacggggatagattccttaaaacaacttgggattactcatgttcagcttatg 1461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               227
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                                                                                                                                                                                                                                                                                                                                                                                                             Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J., Henry,D., Wood,T.C., Leslie,A. and Wilkins,T.A.
An integrated analysis of the genetics, development, and evolution of the cotton fiber
Unpublished (2000)
Contact: Wing RA
Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                             100 Jordan Hall, (Tel: 864 656 7288 Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GA_Ea0026B23 Gossypium arboreum 7-10 dpa fiber library Gossypium arboreum con clone GA_Ea0026B23, mRNA sequence.

AW730507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gossypium arboreum
                                                                                                                                                                                                                                                                                                        Email: rwing@clemson.edu
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1 (bases 1 to 921)
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                                                                                  /db_xref="taxon:29729"
/clone="GA_E80026B23"
/clone_11b="GGssyptum arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-10
/note="Vector: pBK-CMV;
160 c 239 g 20
                                                                                                                                                                                             /organism="Gossypium arboreum"
/strain="AKA"
                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                             /cultivar="8400"
                                           'lab_host="E. coli"
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/; Site_1: EcoRI; Site_2: xhoI"
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nes 153; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Loftus, B., Van Aken, S. and Fraser, C. Determination of clone end sequences HMI: IMSS sheared DNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AZ532406 DNA sequence.
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High quality sequence stop: 812
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                      Email: bjloftus@tigr.org
Clones are derived from
                                                                                                                                                                                                                                                                                                                                                                       9712 Medical Center Dr., Rockville, Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                             Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2000)
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                                                                                                                                                                                                                                                                                                 primer: M13-Forward
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               /clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site_1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to
                                                                                                                                               /organism="Entamoeba histolytica"
/strain="HM1: IMSS"
/db_xref="taxon:5759"
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Pred. No. 3
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Mismatches 134; Indels
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AZ683014/c
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AUTHORS
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             476 GAAATGGTTCAAAAAGCACTTCAAATGATTGAACGTATTAATAAAAGAATGACAAAAATT 417
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ENTHN79TR Entamoeba l
                                                                                                                                                                                                                                                                                                                                       Class: shotgun
High quality sequence start:
High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: bjloftus@tigr.org
Clones are derived from the
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Contact: Brendan J Loftus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 301 838 0200 Fax: 301 838 0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Department of Eukaryotic Genomics
The Institute for Genomic Research
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/Clone_lib-"Entamoeba histolytica Sheared DNA"
/note-"Vector: pHOS1; Site_1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (-2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
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                                                                                                                                                                                                                                     /organism⇒"Entamoeba histolytica"
/strain⇒"HM1:IMSS"
/db_xref~"taxon:5759"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: bjloftus@tigr.org
Clones are derived from the Entamoeba histolytica HMl:IMSS sheared
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2000)
Contact: Brendan J Loftus
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Determination of clone end sequences from Entamoeba histolytica
HM1:IMSS sheared DNA library
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1 (bases 1 to 923)
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              /clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site_l: BSt I; Constructed at The
/note: BST I; Constructed at The
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a 185 c 81 g 416 t
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/db_xref="taxon:5759"
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Pullulanase amino Bacillus deramific Bacillus deramific Trimmed enzyme pro Pullulanase (pulB) Thermotoga maritim Thermotoga maritim Fervidobacterium p
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ALIGNMENTS

RESULT R56990

Bacillus deramificans pullulanase precursor.

21-FEB-1995 (first entry)

R56990;

R56990 standard; Protein; 957 AA

/note- "corresponds to GCN codon" Misc-difference 812 /note= "corresponds to CAN codon" Misc-difference 621 /note= "corresponds to NNA codon" Nisc-difference 620 /note= "corresponds to GGN codon" Misc-difference 164 Location/Qualifiers Bacillus 20-DEC-1993; 06-JUL-1994 28-DEC-1992; EP605040-A. hydrolysis; alpha-1,6-glycosidic bond; starch saccharification Pullulanase; recombinant production; pullulan; amylopectin; deramificans T 89.117D (LMG P-13056). 92BE-0001156 93EP-0203593 /note= "corresponds to ANA codon"

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Query Match
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DNA vectors, transformed cells etc.
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             1999-540851/45.
DB; X87941.
                                                                                                                                                                                                                                                                                                                                                              KAASELHAINPGIALYGEPWTGGTSALPDDQLLTKGAQKGMGVAVFNDNLRNALDGNVFD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 {\tt ssaqg} \, {\tt fatgatgltdaikngvegsindftsspgetinyvtshdnytlwdkialsnpndse}
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                                                                                                                                                                                                                                                                                                                               standard;
                                                                                                                                                                                                                                              deramificans
                                                                                                                                                                                                                                                                 ase; enzyme engineering; starch; saccharification;
chain amylase; alpha-dextrin 6-glucano-hydrolase;
                                Shetty JK;
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783
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135
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592
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of Claim 32
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of Claim 31
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Best Local S
Matches 927
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Local Similarity 99.9%;
Nes 927; Conservative
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                            KHITPKNIEDEVIYEMDVRDFSIDPNSGMKNKGKYLALTEKGTKGPDNVKTGIDSLKQLG
                                                         gvweatvnqnlenwyymyevtgqgstrtavdpyataiapngtrgmivdlaktdpagwnsd
                                                                                                                          rnvlnssqyyysgddlgntytqkattfkvwaptstqvnvllydsatgsvtkivpmtasgh
                                                                                                                                          RNVLNSSQYYYSGDDLGNTYTQKATTFKVWAPTSTQVNVLLYDSATGSVTKIVPWTASGH
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Pred. No. 0;
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Misc-difference 592
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Misc-difference 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; recombinant production; pullulan;
alpha-1,6-glycosidic bond; starch s
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                                                      92BE-0001156.
93BE-0000744.
93BE-0001278.
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Best Local
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         DQLLTKGAQKGMGVAVFNDNLRNALDGNVFDSSAQGFATGATGLTDAIKNGVEGSINDFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DGNTTTTIVHYFCPAGDYQPWSLWWWPXDGGGAEYDFNQPADSFGAVASADIPGNPSQVG
d@lltkgaqkgmgvavfndnlrnaldgnvfdssaqgfatgatgltdaikngvegsindft
                                         ithvqlmpvfasnsvdetdptqdnwgydprnydvpegqyatnangnarikefkemvlslh
                                                                                                                                                    ITHVQLMPVFASNSVDETDPTQDNWGYDPRNYDVPEGQYATNANGNARIKEFKEMVLSLH
                                                                                                                                                                                    khitpkniedevlyemdvrdfsidpnsgmknkgkylaltekgtkgpdnvktgidsikglg
                                                                                                                                                                                                  KHITPKNIEDEVIYEMDYRDFSIDPNSGMKNKGKYLALTEKGTKGPDNYKTGIDSLKQLG
                                                                                                                                                                                                                                    gvweatvnqnlenwyymyevtgqgstrtavdpyataiapngtrgmivdlaktdpagwnsd
                                                                                                                                                                                                                                                GVWEATYNQNLENWYYMYEVTGOGSTRTAVDPYATAIAPNGTRGMIVDLAKTDPAGWNSD
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Pred. No. 0;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                    Pullulanase; debranching enzyme; amylopectin; thermostable; c genetically engineered variant; wheat; potato; wheat; manioc; starch; sugar production; high fructose syrup; high maltose s
                                                                                                                                            Claim
                                                                                                                                                                Variant bacterial pullulanases and isoamylases having, e.g thermostability, used for converting starch from potatoes
                                                                                                                                                                                                      Bisgard-Frantzen H,
                                                                                                                                                                                                                                                                                                                                                                                               Y78514 standard;
                                                                                                                                                                                                                                                   02-JUL-1999;
                                                                                                                                                                                                                                                                                                Bacillus deramificans
                                                                                                                                                                                                                                                                                                                                                   Pullulanase
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                                                                                                                                                                                                                                                                                                                                                                                                                                          GQAEGSVQVPGISMMILHQEVSPDHGKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QFLNSPENTVAYELTDHVNKDKWGNIIVVYNPNKTVATINLPSGKWAINATSGKVGESTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSPGETINYVTSHDNYTLWDKIALSNPNDSEADRIKMDELAQAVVMTSQGVPFMQGGEEM
                                                                                                                                                                                         2000-160767/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                  gqaegsvqvpgismmilhqevspdhgkk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qflnspentvayeltdhvnkdkwgnlivvynpnktvatinlpsgkwainatsgkvgestl
                                                                                                                                            29;
                                                                                                                                            Fig
                                                                                                                                                                                                                                                                                                                                                   amino
                                                                                                                                           3; 116pp; English.
                                                                                                                                                                                                                                                    99WO-DK00381
                                                                                                                                                                                                                                                                                                                                                                                               protein;
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This sequence represents a pullulanase amino acid sequence. Pullulanases CC are debranching enzymes which can attack amylopectin. This sequence represents a parent enzyme from which genetically engineered variant CC debranching enzymes can be created. The genetically engineered to the CC an improved thermostability at a pH in the range of 4-6 compared to the CC parent enzyme. The modified enzyme may alternatively or also have an CC increased activity towards amylopectin and or glycogen compared to the CC parent enzyme. This is useful when starches yeth as corn, potato, wheat, CC manioc and rice starch are used as starting materials in commercial CC large scale production of sugars, such as high fructose syrup, high maltose syrup, maltodextrins, amylose, G4-66 oligosaccharides and other CC carbohydrates such as fat replacers. The thermostable debranching enzymes of the invention make it possible to perform liquefaction and debranching the thermostable debranching using the thermostable debranching using the thermostable debranching using the with the action of an alpha-amylase, the formation of panose precursors ci is reduced, thereby reducing the panose content in the final product and

increasing

overall saccharification yield.

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                                                                                                                                                             VIPRNVLNSSQYYYSGDDLGNTYTQKATTFKVWAPTSTQVNVLLYDSATGSVTKIVPMTA 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DGNTTTIIVHYFCPAGDYQPWSLWMWPKDGGGAEYDFNQPADSFGAVASADIPGNPSQVG 89
                                                  SHLQFLNSPENTVAYELTDHVNKDKWGNIIVVYNPNKTVATINLPSGKWAINATSGKVGE
                                                                                                                     OLGITHVQLMPVFASNSVDETDPTQDNWGYDPRNYDVPEGQYATNANGNARIKEFKEMVL
                                                                                                                                                                                                                                                                                                                                          NSDKHITPKNIEDEVIYEMDVRDFSIDPNSGMKNKGKYLALTEKGTKGPDNVKTGIDSLK 505
                                                                                                                                                                                                                                                                                                                                                                                   SGHGVWEATVNQNLENWYYMYEVTGQGSTRTAVDPYATAIAPNGTRGMIVDLAKTDPAGW
                                                                                                                                                                                                                                                                                                                                                                                                                viprnvlnssqyyysgddlgntytqkattfkvwaptstqvnvllydsatgsvtkivpmta
                                                                                       EEMLRXKGGNDNSYNAGDAVNEFDWSRKAQYPDVFNYYSGLIHLRLDHPAFRMTTANEIN
                                                                                                                                                                                                                                                                                      qlgithvqlmpvfasnsvdetdptqdnwgydprnydvpegqyatnangnarikefkemvl
                                                                                                                                                                                                                                                                                                                                                                        sghgvweatvnqnlenwyymyevtgqgstrtavdpyataiapngtrgmivdlaktdpagw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              apdnhstllkkvtnnlyqfsgdlpegnyqykvamshs---aqpvtsvqavwpgrpyplga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APDNHSTLLKKYTNNLYQFSGDLPEGNYQYKVALNDSWNNSYPSDNINLTVPAG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dgntttiivhyfrpagdyqpwslwmwpkdgggaeydfnqpadsfgavasadipgnpsqvg 60
         STLGQAEGSVQVPGISMMILHQEVSPDHGKK 956
                                                                                                                                                                                                                           OKFIIDSLKYWVNEYHIDGFRFDLMALLGKDTMSKAASELHAINPGIALYGEPWTGGTSA
                                                                                                                                                                                                                                                                                                                               nsdkhitpkniedeviyemdvrdfsidpnsgmknkgkylaltekgtkgpdnvktgidslk
stlggaegsvqvpgismmilhgevspdhgkk 915
                                        <u>shlqflnspentvayeltdhvnkdkwgniivvynpnktvatinlpsgkwainatsgkvge</u>
                                                                                eemlrtkggndnsynagdavnefdwsrkagypdvfnyysglihlrldhpafrmttanein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 866;
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93.0%;
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Pred. No. 6.3e-297;
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pullulanase of Bacillus deramificans strain T89.117D, comprising CC amino acids 99-928 of the native mature enzyme (see Y31746). The cathor and in a companies of the native mature enzyme (see Y31746). The cc mature pullulanase (EC-3.2.1.41) has a pI of 4.1-4.5, a cc half-life of about 55 hr at 60 deg C and is capable of catalysing CC the hydrolysis of alpha-1,6-glucosidic bonds in amylopectin and cc pullulan. The invention relates to the discovery that B. C deramificans pullulanase recombinantly produced in a Bacillus host is modified yet retains the ability to catalyse the hydrolysis of CC is modified yet retains the ability to catalyse the hydrolysis of CC an alpha-1,6-glucosidic bond. The modification of the recombinant cc pullulanase appears to be a result of misprocessing of the signal CC sequence by a signal peptidase as well as susceptibility to sequence by a signal peptidase as well as susceptibility to cxtracellular proteolytic processing. The invention provides CC modified pullulanases, especially N-terminally truncated B. CC deramificans modified pullulanases, nucleic acids encoding them, CC vectors, host cells and methods for recombinant production. The condified pullulanases are useful in the starch industry for the saccharification of aqueous liquefied starch, forming syrups of CC anti-staling additives in bread; in brewing low calorie beers; corrected of carrier of fruit in the starch calorie beers; in the preparation of
industry
modified
                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents an N-terminally truncated pullulanase of Bacillus deramificans strain T89.117D, com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note-
Misc-difference 591
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                                              for fat); to clarify fruit juices; in the preparation of oligosaccharides from amylopectin or of tetraholosides f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New modified pullulanase for saccharification of aqueous liquefied
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-540851/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-MAR-1999;
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            to condense mono- or oligosaccharides, or in the pharmaceutical industry (no details). When used for starch saccharification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GEMV ) GENENCOR INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        deramificans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page -;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shetty JK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           enzyme engineering;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0034630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US04627
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592
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783
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-truncated pullulanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "encoded by GGN"
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Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   they provide higher glucose yields in short reaction times, without losses associated with reversion reaction products. When used with glucoamylase, they make possible a higher level of dissolved solids in the material being treated, resulting in increased productivity and a more energy-efficient process.

Note: The present sequence is not shown in the specification but is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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IHLRLDHPAFRWTTANEINSHLQFLNSPENTVAYELTDHVNKDKWGNIIVVYNPNKTVAT
                                                                                                                elaqavvmtsqgvpfmqggeemlrxkggndnsynagdavnefdwsrkaqypdvfnyysgl
                                                                                                                                                                                             TGATGLTDAIKNGVEGSINDFTSSPGETINYVTSHDNYTLWDKIALSNPNDSEADRIKMD
                                                                                                                                                                                                                                       ainpgialygepwtggtsalpddglltkgaqkgmgvavfndnlrnaldgnvfdssaqgfa
                                                                                                                                                                                                                                                      AINPGIALYGEPWTGGTSALPDDQLLTKGAQKGMGVAVFNDNLRNALDGNVFDSSAQGFA
                                                                                                                                                                                                                                                                                                 iiptdqvlemklxaerpmvqkf1idslkywvneyhidgfrfdlmallgkdtmskaaselh
                                                                                                                                                                                                                                                                                                              IIPTDQVLEMKLXAERPMVQXFIIDSLXYMVNEYHIDGFRFDLMALLGKDTMSKAASELH
                                                                                                                                                                                                                                                                                                                                                      PNGTRGMIVDLAKTDPAGWNSDKHITPKNIEDEVIYEMDVRDFSIDPNSGMKNKGKYLAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dpdvshtlsiqtdgyqakqv1prnv1nssqyyysgdd1gntytqkattfkvwaptstqvn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DPDVSHTLSIQTDGYQAKQVIPRNVLNSSQYYYSGDDLGNTYTQKATTFKVWAPTSTQVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INLPSGKWAINATSGKVGESTLGQAEGSVQVPGISMMILHQEVSPDHGKK 956
                                                                                                                                                ELAQAVVMTSQGVPFMQGGEEMLRXKGGNDNSYNAGDAVNEFDWSRKAQYPDVFNYYSGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           \verb"pngtrgmlvdlaktdpagwnsdkhltpknledevlyemdvrdfsldpnsgmknkgkylal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LGQDVTAVLAGTFQHIFGGSDWAPDNHSTLLKKVTNNLYQFSGDLPEGNYQYKVALNDSW
                                                                                                                                                                            tgatgltdalkngvegsindftsspgetinyvtshdnytlwdkialsnpndseadrikmd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from the B. deramificans pullulanase sequence given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              830
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99.9%;
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Pred. No. 2.5e
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RESULT
Y31748
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Misc-difference 591
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                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                  New modified pullulanase for saccharification of aqueous liquefied
                                                                                                                                                             WPI; 1999-540851/45
                                                                                                                                                                      Miller
                                                                                                                                                                                        04-MAR-1998;
                                                                                                                                                                                                 03-MAR-1999;
                                                                                                                                                                                                                     WO9945124-A2
                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                       Bacillus deramificans
                                                                                                                                                                                                                                                                                                      Pullulanase;
                                                                                                                                                                                                                                                                                                                                   Y31748;
                                                                                                                                                                                                                                                                                                                                           Y31748 standard; Protein;
                                                                                                                                                                               (GEMV
                                                                                                                                                                                                                                                                                                                         22-NOV-1999
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                                                                                                                                                                               ) GENENCOR INT
                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                     enzyme engineering; starch; saccharification;
                                                                                                                                                                                                                                  /note=
, 783
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                                                                                                                                                                                                 99WO-US04627
                                                                                                                                                                                                                                            /note-
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                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                    note-
                                                                                                                                                                                                                                                                                                               N-truncated
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Claim 32; Page -; 49pp; English

The present sequence represents an N-terminally truncated CC pullulanase of Bacillus deramificans strain TB9:117D, comprising CC amino acids 103-928 of the native mature enzyme (see Y31746). The CC native mature pullulanase (EC-3,2.1.41) has a pI of 4.1-4.5, a cC thalf-life of about 55 hr at 60 deg C and is capable of catalysing CC the hydrolysis of alpha-1.6-glucosidic bonds in amylopectin and CC pullulan. The invention relates to the discovery that B. CC is modified yet retains the ability to catalyse the hydrolysis of CC an alpha-1.6-glucosidic bond. The modification of the recombinant CC pullulanase appears to be a result of misprocessing of the signal complete by a signal peptidase as well as susceptibility to extracellular proteolytic processing. The invention provides CC deramificans modified pullulanases, especially N-terminally truncated B. CC deramificans modified pullulanases, nucleic acids encoding them, CC vectors, host cells and methods for recombinant production. The CC saccharification of aqueous liquefied starch, forming syrups of CC anti-staling additives in bread; in browing low calorie beers; CC anti-staling additives in bread; in browing low calorie beers; CC condense and maliose content. Other uses (not claimed) are: as CC condense mono- or oligosaccharides, or in the pharmaceutical CC industry (no details). When used for starch saccharification, the CC condense mono- or oligosaccharides, or in the pharmaceutical CC industry (no details). When used for starch saccharification, the CC they provide higher glucose yields in short reaction times, without as substitute maltose;

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Best Local Similarity
Matches 825; Conserv
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Note: The present sequence is not shown in the specification derived from the B. deramificans pullulanase sequence given is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                      911
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                                                                                                                                                                                                     GIALYGEPWIGGTSALPDDQLLIKGAQKGMGVAVFNDNLRNALDGNVFDSSAQGFATGAT
                                                                                                                                                                                                                                                                                                                                                                               DSATGSVTKIVPMTASGHGVWEATVNQNLENWYYMYEVTGQGSTRTAVDPYATAIAPNGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EDAAKPAVSNAYLDASNQVLVKLSQPLTLGEGXSGFTVHDDTANKDIPVTSVKDASLGQD
SGKWAINATSGKVGESTLGQAEGSVQVPGISMMILHQEVSPDHGKK 956
                                                LDHPAFRTTANEINSHLOFLNSFENTVAYELTDHVNKDKWGNIIVYVNHVKTVATINLP
                                                                                                                                  GLTDALKNGVEGSINDFTSSPGETINYVTSHDNYTLWDKIALSNPNDSEADRIKMDELAQ
                                                                                                                                                                                                                                                                                                                              RGMIVDLAKTDPAGWNSDKHITPKNIEDEVIYEMDVRDFSIDPNSGMKNKGKYLALTEKG
                                                                                                                                                                                                                                                                                                                                                                                                            shtlsiqtdgygakqviprnvlnssqyyysgddlgntytqkattfkvwaptstqvnvlly
                                                                                                                                                                                                                                                                                                                                                                                                                       SHTLSIQTDGYQAKQVIPRNVLNSSQYYYSGDDLGNTYTQKATTFKVWAPTSTQVNVLLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          \verb|vtavlagtfqhifggsdwapdnhstllkkvtnnlyqfsgdlpegnyqykvalndswnnps||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   edaakpavsnayldasnqvlvklsqpltlgegxsgftvhddtankdipvtsvkdaslgqd 60
                                                                                                                       gltdaikngvegsindftsspgetinyvtshdnytlwdkialsnpndseadrikmdelag
                                                                                                                                                               gialygepwtggtsalpddqlltkgaqkgmgvavfndnlrnaldgnvfdssaqgfatgat
                                       dsatgsvtkivpmtasghgvweatvnqnlenwyymyevtgqgstrtavdpyataiapngt
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99.98;
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Pred. No. 5.6e-284;
0; Mismatches 0;
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Best Local S
Matches 772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus sp. APC heat resistance;
                                                                                                                                                                                                                                                                      The present sequence represents a trimmed enzyme isolated from Bacillus sp. APC-9603. The present specification also describes: (1) a vector containing the DNA encoding a trimmed enzyme; (2) a recombinant microbe transformed by the DNA; and (3) preparation of a trimmed enzyme in which the microbe of (2) is cultured and the trimmed enzyme is collected from the culture. The method can prepare a trimmed enzyme of wide substrate specificity having heat resistance and being active in acid region efficiently.
                                                                                                                                                                                                                                                                                                                                                                 enzyme
                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W37372 standard;
                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                 Claim
                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                (AMAN ) AMANO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Trimmed
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DB; T97233.
                                              DGNTTTIIVHYFCPAGDYQPWSLWMWPKDGGGAEYDFNQPADSFGAVASADIPGNPSQVG
GVWEATVNQNLENWYYMYEVTGQGSTRTAVDPYATAIAPNGTRGMIVDLAKTDPAGWNSD
                                                                                                                                                                               dgtttnvivhyfrpggdygswslwmwpeggdgnnynfn-gtdsygeianvsipgspskvg
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wide
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                                                                                                                                                                                                                                                                                                                                                                 substrate
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83.7%;
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                                                                                                                                                                                                                                                                                                                                                                 specificity
                                                                                                                                                                                                                Score 4148; DB 19;
Pred. No. 4.9e-272;
3; Mismatches 85;
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Variant bacterial pullulanases and isoamylases having,
                                                                                                                                                                                                               Pullulanase; pulB; debranching enzyme; amylopectin; thermostable; corn; genetically engineered variant; wheat; potato; wheat; manioc; rice; genetically engineered variant; wheat; potato; wheat; manioc; rice; starch; sugar production; high fructose syrup; high maltose syrup;
                       N-PSDB; Z89960
                                                    Bisgard-Frantzen H,
                                                                                                                                                                                                                                                                                  05-MAY-2000
                                                                                                                                                                                                                                                                                                         Y78513
                                                                          (NOVO ) NOVO-NORDISK
                                                                                                02-JUL-1998;
                                                                                                                      02-JUL-1999;
                                                                                                                                           13-JAN-2000
                                                                                                                                                               W0200001796-A2
                                                                                                                                                                                    Bacillus acidopullulyticus
                                                                                                                                                                                                                                                             Pullulanase
                                                                                                                                                                                                                                                                                                                           Y78513 standard; protein;
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                                                                                                                                                                                                                                                            (pulB) amino acid sequence.
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CC This sequence represents a pullulanase amino acid sequence. Pullulanases CC are debranching enzymes which can attack amylopectin. This sequence CC represents a parent enzyme from which genetically engineered variant CC debranching enzymes can be created. The genetically engineered variant CC an improved thermostability at a pH in the range of 4-6 compared to the CC parent enzyme. The modified enzyme may alternatively or also have an CC increased activity towards amylopectin and or glycogen compared to the CC parent enzyme. The enzyme variants are useful for converting starch to one CC or more sugars. This is useful when starches such as corn, potato, wheat, CC manioc and rice starch are used as starting materials in commercial CC large scale production of sugars, such as high fructose syrup, high high carbohydrates such as fat replacers. The thermostable debranching enzymes CC of the invention make it possible to perform liquefaction and debranching simultaneously before the saccharification step. By debranching using the CC with the action of an alpha-amylase, the formation of panose precursors is reduced, thereby reducing the panose content in the final product angular concerning the overall saccharification yield.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 29; Fig 3; 116pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          thermostability, used for converting starch from potatoes
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Sequence

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B Ş 몽 Ş 밁 ş Б Ş 밁 Ş 밁 ð 밁 õ 밁 Ş QY 망 В Ş Query Match Best Local Similarity Matches 451 486 426 195 391 3 3 1 211 193 133 271 306 246 186 74 67 10 LSYCLVLTWAFNVKGQSAHADGNTTTIIVHYFCPAGDYQPWSLWMW---PKDGGGAEYDF LTEKGTKGPDNVKTGIDSLKQLGITHVQLMPVFASNSVDETDPTQDNWGYDPRNYDVPEG APNGTRGMIVDLAKTDPAGWNSDKHITPKNIEDEVIYEMDVRDFSIDPNSGMKNKGKYLA qlllynsetgpvtkqlemqksdngtwklkvpgnlknwyylyqvtvngktqtavdpyvral ayattpegtaritqlkqliqsihkdriainmdvvynhtfnvgvsdfdkivpqyyyrtdsa QYATNANGNARIKEFKEMVLSLHREHIGVUMDVVYNHTFATQISDFDKIVPEYYYRTMIQ svnatrgmivdledtnppgwkedhqqtpanpvdevlyevhvrdfsidansgmknkgkyla NVLLYDSATGSVTKIVPMTASGHGVWEATVNQNLENWYYMYEVTGQGSTRTAVDPYATAI 425 ASIGODVTAVLAGTFQHIFGGSDWAPDNHSTLLKKVTNNLYQFSGDLPEGNYQYKVALND YNEKDAEDAAKPAVSNAYLDASNQVLVKLSQPLTLGEGXSGFTVHDDTANKDIPVTSVKD 185 SWNNSYPSDNINLTVPAGGAHVTFSYIPSTHAVYDTINNPNADLQVESGVKTDLVTVTLG s-gkddfgvkadvqvpgddtqvglivrtndwsqkntsddlhidltkgheiwivqgdpniy 132 NQPADSFGAVASADIPGNPSQVGIIVRTQDWT-KDVSADRYIDLSKGNEVWLVEGNSQIF 129 ftehgtkgpdnvktgidslkelglnavglqpieefnsldetqpnmynwgydprnynvpeg ynlsdagaaatpkvsnayldnektvlakltnpmtlsdgssgftvtdkttgegipvtaatn 192 524: Conservative 54.0%; Score 2732.5; DB 21; 55.3%; Pred. No. 2.3e-176; 105; Mismatches -----sassseqtdlvqltla 203; Indels 115; Length 862; ------Gaps 485 450 510 545 390 330 270 365 210 305 245 99 194 ភូ

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VIIPTDQVLEMKLXAERPMVQKFIIDSLKYWVNEYHIDGFRFDLMALLGKDTMSKAASEL

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This is the amino acid sequence of pullulanase 6GP3, deduced from an isolated polynucleotide (see v36920) of a Thermotoga maritima clone (5GP3) that grows optimally at 85 degC. The sequence shows 72% amino acid identity to an alpha destrom 6 glucanohydrolase of Caldocellum saccharolyticum. The invention provides 18 polynucleotides (see v36907-24) coding for thermostable glycosidases (see w49858-75) having glucosidase, alpha-galactosidase, beta-mannastable glycosidases beta-galactosidase, beta-mannases, endoglucanase or pullulanase activity. Vectors and host cells are also claimed. A method is provided for producing the enzymes by recombinant techniques. A claimed method for generating glucose from soluble
                                                                                                                                                                                                                                                                                                                                                                                               Glycosidase enzymes from organisms of the genera Staphlothermus, Pyrococcus and Thermococcus - for deriving sugar from oligosaccharides, useful in the e.g. food processing, textile or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
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06-DEC-1996;
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Best Local Similarity 36.1
Matches 326; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cell oligosaccharides comprises contacting a sample (selected from dairy products, fruit juice, detergent, textile, guar gum, animal feed, plant biomass or waste product) containing oligosaccharides (selected from maltose, cellobiose, lactose, sucrose, raffinose, stachyose, verbascose, cellulose, starch, amylose, glycogen, disaccharides, polysaccharides and pullulan) with one of the claimed glycosidases such that glucose is produced.
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                         erklqfidvfnyhkgliklrkehpafriknaeeikkhleflpggrrivafmlkdhaggdp
                                                   SRKAQYPDVFNYYSGLIHLRLDHPAFRMTTANEINSHLQFLNSPENTVAYELTDHVNKDK 890
                                                                              adkkkewteeelknaqklagailltsqgvpflhggqdfcrttnfndnsynapisingfdy
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138; Mismatches
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New thermostable glycosidase(s) - from Thermococcus, Staphylothermus and Pyrococcus, used in the textile, food processing, pharmaceutical, detergent and baking industries
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N-PSDB;
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NYTLWDKIALSNPNDSEA----DRIK-MDELAQAVVMTSQGVPFMQGGEEMLRXKGGNDN | :|| | | | ::| | | ::| | ::| | ::|
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                                                                   LRNALDGNVFDSSAQGFATGATGLTDATKNGVEGS----INDFTSSPGETINYVTSHD
                                                                                                qmglmdkvtmlaikselskiepsvvlygepwggwgapi----rfgkadvggtgiaafnde
                                                                                                                              LMALLGKDTMSKAASELHAINPGIALYGEPWTGGTSALPDDQLLTKGAQKGMGVAVFNDN 708
                                                                                                                                                                                                                NKGKYLALTEKGTKGPDNVKTGIDSLKQLGITHVQLMPVFASNSVDETDPTQD---NWGY 535
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                                        frdalrgsvfnatvkgflmgalaketgvkrgvagsieydevirsfakdpgetinyvevhd
                                                                                                                                                                                                                                                                           nkalylgltekgtrgpngvttgldhlvelgvthvhllpmfdfwtgdeadkdfersynwgy 428
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P-PSDB;
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Plasmid pTPI conty. the pullanase gene (Japan Patent Apppln. No. 174037/88) was cleaved by various restriction enzymes and inserted into plasmid pVI18/119. Single-stranded DNA was prepd. using helper phage M13K07 and the base sequence determined by the dideoxy method.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence encoding this protein may plasmid. The heat-resistant pullanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; Page 2-3; 8pp; Japanese.
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Best Local Similarity
Matches 284; Conserv
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                                                                                                nigflvlnttngdkd-ggdkavelfspdlneiwikggsdevflyepvdlpantvrihyer
                                                                                                                           QVG-IIVRTQDWTKDVSADRYIDLSKG--NEVWLVEGNSQIF-------
                         SGFTVHDDTANKDIPVTSVKDASLGQ--DVTAVLAGTFQHIF--GGSDWAPDNHSTLLKK 220
                                                 tnadyegwglwnwedvespsdgwpngaadaagigkygayyd-----iklk------
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                                                                          --YNEKDAE-----
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W09255 standard;

Protein; 1938

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Amylopullulanase; alpha-amylase; pullulanase;

detergent additive.

Bacillus alkaline amylopullulanase.

27-MAR-1997

(first entry)

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Bacillus

KSM-AP1378

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Amylopullulanase (W09255) of Bacillus sp. isolate KSM-AP1378 has N-terminal alkaline alpha-amylase molety (see also W09256) and a C-terminal alkaline pullulanase molety (see also W09257). It is the product of an open reading frame in a DNA fragment (T47878) isolated using shotgun cloning and PCR (see also T47879-84). The
                                                                  DNA encoding alkaline pullulanase having alkaline alpha-amylase activity - useful for improving the efficacy of dish washing detergents and detergents for clothes, esp. on starch soils
                                 Amylopullulanase (W09255) of Bacillus sp.
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                                                     Disclosure;
                                                                                                        N-PSDB;
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/note= "amylase
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1: /cgn2_6/ptodata/2
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4: /cgn2_6/ptodata/2
5: /cgn2_6/ptodata/2
6: /cgn2_6/ptodata/2
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     April 22, 2001, 07:58:36; Search time 51.08 Seconds (without alignments) 359.545 Million cell updates/sec
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US-08-39-715A-1 US-08-339-715A-3 US-08-339-715A-3 US-08-339-715A-3 US-08-339-715A-3 US-08-607-321-4 US-08-607-321-4 US-08-607-321-14 US-08-605-501-14 US-08-374-155A-4 US-08-374-155A-10 US-08-374-155A-4 US-08-374-155A-4

ALIGNMENTS

Sequence 11, Application US/08474140 Patent No. 5721127 GENERAL INFORMATION: APPLICANT: ADMER, PHILIPPE APPLICANT: ADMER, ANTOINE TITLE OF INVENTION: PULLULANASE, MICROORGANISMS WHICH TITLE OF INVENTION: PULLULANASE, AND THE USES THEREOF NUMBER OF SEQUENCES: 15 CORRESPONDENCE ADDRESS: ADDRESSEE: WILLIAN BRINKS HOPER GILSON & LIONE, P.C. STATE: D.C. SOUTHY: WASHINGTON SOUTHARB: PEODS/MS-DOS SOUTHARB: PEODS/MS-DOS SOUTHARB: PEODS/MS-DOS SOUTHARB: D.C. APPLICATION NUMBER: US/08/474,140 FILLING DATE: 07-JUN-1995 CLASSIFICATION NUMBER: 37,136 REFERENCE/DOCKET NUMBER: 37,136 REFERENCE/DOCKET HOPBARTION: TELEPONNUSCATION INFORMATION: TELEPONNUSCATION INFORMATION: TELEPONNES (202) 429-0625 TELEFAX: (202) 429-0625 TELEFAX: (202) 293-1850 TELEFAX: (202) 293-1850 TELEFAX: (202) 293-1850 TELEFAX: (202) 293-1850 TELEFAX: (202) 429-0625 TELEFAX: (202) 429-0625

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30 DGNTTTIIVHYFCPAGDYQPWSLWMWPKDGGGAEYDFNQPADSFGAVASADIPGNPSQVG

Query Match Best Local S Matches 926

Local Similarity 99.8 mes 926; Conservative

96.6%;

; Score 4888.5; Pred. No. 0; 1; Mismatches

DB 1; 0;

928; 1;

Length Indels

Gaps VG 89

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RESULT 2
US-08-477-630-11
                                               Sequence 11, Application Patent No. 5721128 GENERAL INFORMATION:
APPLICANT: DEWEER, PHILIPPE
APPLICANT: AMORY, ANTOINE
TITLE OF INVENTION: PULLULANASE, MICROORGANISMS WHICH
TITLE OF INVENTION: PRODUCE IT, PROCESSES FOR THE PREI
TITLE OF INVENTION: PULLULANASE AND THE USES THEREOF
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APPLICATION UMBER: US/08/477,630
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT IMPORMATION: Esq.
NAME: WILHLEM F. Gadiano, Esq.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-42
TELECOMMUNICATION INFORMATION:
TELEPAN: (202) 429-0625
TELEFAN: (202) 293-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 928 amino acids
TYPE: amino acids
TYPE: annino acids
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CORRESPONDENCE ADDRESS:
CORRESPECT: WILLIAN HRINKS HOFER GILSON
STREET: 2000 K Street, N.W., Suite 200
CITY: Washington
STATE: D.C.
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SOFTWARE: Patentin Reli
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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les 926; Conserv
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                                                                   FSYIPSTHAVYDTINNPNADLQVESGVKTDLVTVTLGEDPDVSHTLSIQTDGYQAKQVIP FSYIPSTHAVYDTINNPNADLQVESGVKTDLVTVTLGEDPDVSHTLSIQTDGYQAKQVIP
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TELEFAX: (202) 429-0625
TELEFAX: (202) 293-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 928 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: protein
008-472-293-11
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                          ADDRESSEE: WILLIAN BRINKS HOPER GILSON & LIC
STREET: 2000 K Street, N.W., Suite 200
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,293
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
NAME: WILhlem F. Gadlano, Esq.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: DEWEER, PHILIPPE
APPLICANT: AMORY, ANTOINE
TITLE OF INVENTION: PULLULAN
TITLE OF INVENTION: PULLULAN
TITLE OF INVENTION: PULLULAN
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         GQAEGSVQVPGISMMILHQEVSPDHGKK 956
                                 DQLLTKGAQKGMGVAVFNDNLRNALDGNVFDSSAQGFATGATGLTDAIKNGVEGSINDFT
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GQAEGSVQVPGISMMILHQEVSPDHGKK 928
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Sequence

Application

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REFERENCE/DOCKET NUMBER: 4121-43

TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-0625
TELEPHONE: (202) 293-1850
TELEFAX: (202) 293-1850
TELEX: (500) 383-5605
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 928 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 926; Conserv
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GENERAL INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHTIN Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,545
FILING DATE: 07-JUN-1995
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TITLE OF INVENTION: PRODUCE TT, PROCESSES FOR THE PRI
TITLE OF INVENTION: PULLULANASE AND THE USES THEREOF
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ATTORNEY/AGENT INFORMATION:
NAME: Wilhlem F. Gadiano,
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CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
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GWEATUNGNLENWYYMYEUTGQGSTRTAVDPYATAIAPNGTRGMIVDLAKTDPAGWNSD
                 GVWEATVNQNLENWYYMYEVTGGGSTRTAVDPYATA1APNGTRGMIVDLAKTDPAGWNSD
                                                                RNVLNSSQYYYSGDDLGNTYTQKATTFKVWAPTSTQVNVLLYDSATGSVTKIVPMTASGH 388
                                                                                                                                APDNHSTLLKKVTNNLYQFSGDLPEGNYQYKVALNDSWNN-SYPSDNINLTVPAGGAHVT
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    INFORMATION
                                                 NAME: Wilhlem F. Gadlano, Esq. REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-45
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: DEWEER, PHILIPPE
APPLICANT: AMORY, ANTOINE
TITLE OF INVENTION: PULLULANASE, MICROORGANISMS WHICH
TITLE OF INVENTION: PRODUCE IT, PROCESSES FOR THE PREPARATION OF THIS
TITLE OF INVENTION: PULLULANASE AND THE USES THEREOF
                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Wilhlem F. Gadiano,
                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
TELEFAX: (202) 293-1850
TELEX: 650 383-5605
DRMATION FOR SEQ ID NO: 1
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                                           (202) 429-0625
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SEQUENCE CHARACTERISTICS: LENGTH: 928 amino acid

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Best Local Similarity
Matches 926; Conserv
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TOPOLOGY: linear
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GQAEGSVQVPGISMMILHQEVSPDHGKK
                            QFLNSPENTVAYELTDHVNKDKWGNIIVVYNPNKTVATINLPSGKWAINATSGKVGESTL
                                                      LRXKGGNDNSYNAGDAVNEFDWSRKAQYPDVFNYYSGLIHLRLDHPAFRMTTANEINSHL
                                                               LRXKGGNDNSYNAGDAVNEFDWSRKAQYPDVFNYYSGLIHLRLDHPAFRMTTANEINSHL
                                                                                           SSPGETINYVTSHDNYTLWDKIALSNPNDSEADRIKMDELAQAVVMTSQGVPFMQGGEEM
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                 QFLNSPENTVAYELTDHVNKDKWGNIIVVYNPNKTVATINLPSGKWAINATSGKVGESTL
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Pred. No. 0;
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FILING DATE: 19-NOV-1993
PRIOR APPLICATION NUMBER: BE 09300744
FILING DATE: 15-JUL-1993
PRIOR APPLICATION NUMBER: BE 09300744
FILING DATE: 15-JUL-1993
PRIOR APPLICATION NUMBER: BE 09201156
FILING DATE: 28-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Debra J. Glaister, Esq.
REGISTRATION NUMBER: 33,888
REFERENCE/DOCKET NUMBER: GC446C1-US
TELECOMMUNICATION: TOFORMATION:
TELEPHONE: (650) 846-7620
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 928 amino acids
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Patent No. 6
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,733
FILING DATE: 23-DEC-1997
PRIOR APPLICATION NUMBER: US 08/472,293
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 08/174,893
FILING DATE: 28-DEC-1993
PRIOR APPLICATION NUMBER: US 08/174,893
PRIOR APPLICATION DATA:
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Best Local Similarity
Matches 926; Conserv
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ADDRESSEE: Genencor International,
STREET: 925 Page Mill Road
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TITLE OF INVENTION: PRODUCE IT, PROCESSES FOR THE PR
TITLE OF INVENTION: PULLULANASE AND THE USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: DEWEER, PHILIP APPLICANT: AMORY, ANTOINE
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TYPE: amino acids
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Pred. No. 0;
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APPLICANT: KOSSMANN, Jens
APPLICANT: Emmermann, Michael
APPLICANT: Virgin, Ivar
APPLICANT: Renz, Andreas
TITLE OF INVENTION: DNA MOLECULES CODING FOR
TITLE OF INVENTION: FROM PLANTS
FILE REFERENCE: AGREVO-6
CURRENT APPLICATION NUMBER: US/08/860,339
CURRENT FILING DATE: 1997-11-25
EARLIER APPLICATION NUMBER: DE P4447387.7
EARLIER FILING DATE: 1994-12-22
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US-08-860-339-18
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SNWPLIKKRLANPSYKPDKNHIIAAVENFTNLLQIRYSSPLFRLRSAKDIEDRVRFHNNV
                                                                                 AQAVVMTSQGVPFMQGGEEMLRXKGGNDNSYNAGDAVNEFDWS------
                                                                                                                                           ------FTSSPGETINYVTSHDNYTLWDKIALSNPNDSEAD-RIKMDEL
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                                                                                                                 KQVKGSEVYTYGGTPVGYAMQPIETINYVSAHDNETLFDIVSLKTPTYITVDERCRVNHL
                                                        ATSILALSQGIPFFHAGDELLRSKSLDRDSYNSGDWFNRLDFSYNSNNWGVGLPPKDHNE
                            ----RKAQYPD-----VFNYYSGLIHLRLDHPAFRMTTANEINSHLQFLNSP
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Pred. No. 8e-52;
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                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 149; Conserv
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GENERAL INFORMATION:
APPLICANT: Choi et. al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (301) 309-8512
INFORMATION FOR SEO ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 618 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
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NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                    507 LGITHVQLMPVFASNSVDE------TDPTQDNWGYDPRNYDVPEGQYATN-ANGN 554
                                    675 YGEPWTGGTSALPDDQLLTKGAQKGM-----GVAVFNDNLRNALDGNVFDSSAQGFATGA 729
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OPERATING SYSTEM:
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CITY: Rockville
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                                                                          GGRLGTTHHMTKRLLIDSIKYLVDTYKVDGFRFDMMGDHDAASIEEAYKAARALNPNLIM 177
                                                                                                              EMKLXAERPMVQKFIIDSLKYWVNEYHIDGFRFDLMALLGKDTMSKAASELHAINPGIAL 674
LGEGW----RTYAGDENMPTKAADQDWMKHTDTVAVFSDDIRNNLKSGYPNEGQPAFITGG
                                                                                                                                                      KRIAEFKNLINEIHKRGMGAILDVVYNHT--AKVDLFEDLEPNYYH-FMDADGTPRTSFG
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                                                                                                                                                                                                                                                                                                                              Score 543; DB 4; Length 618; Pred. No. 2.9e-34;
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GENERAL INFORMATION:
                                                                                                          Matches 191;
                                                                                                                                          Query Match
Best Local :
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INFORMATION FOR SEQ
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 32,963
REFERENCE/DOCKET NUMBER: 38
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 746 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 28-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bonner, Grace L.
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
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344 LGNTY--TOKATTFKVWAPTSTQVNVLLYDSATGS--VTKIVPMTASGHGVWEATV-NQN 398
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TOPOLOGY: linear
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STREET: 700 Chesterfield Parkway No. 5750876th
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                                                                                                                                          Similarity
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                                                                                                          Score 509; DB 1;
Pred. No. 1.8e-31;
Nismatches 290
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RESULT 10
PCT-US95-09323-11
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                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
APPLICATION NUMBER: US 0
FILING DATE: 28-JUL-1994
INFORMATION FOR SEQ ID NO: 1
                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
          SEQUENCE
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CLASSIFICATION:
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          CHARACTERISTICS:
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Containing It and Methods
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US-08-476-519-2
US-08-476-519-2
Sequence 2, Application US/08476519
Patent No. 5750876
GENERAL INFORMATION:
APPLICANT: Barry, Gerard F.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Krohn, Bradley M.
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; TYPE: manino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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INFORMATION FOR SEQ ID NO:
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FILING DATE: 28-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bonner, Grace L.
REGISTRATION NUMBER: 32,963
REFERENCE/DOCKET NUMBER: 38-21(13577)A
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CORRESPONDENCE ADDRESS:
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LENGTH: 777 amino acids
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APPLICATION NUMBER: US
FILING DATE:
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MEDIUM TYPE: Floppy disk
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Local Similarity 25.5%; Pred. No. 1.9e-31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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STREET: 700 Chesterfield Parkway No. 5750876th
                                                                                       QKFIIDSLKYWVNEYHIDGFRFDLMALLGK---
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                      AINPGIALYGEPWT-GGTSALPDDQLLTKGAQKG---MGVAVFNDNLRNALDGNVFDSSA
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AGGAGADLIAEPWAIGGNS----
                                                                  QNLIVDSLAYWRDALGVDGFRFDLASVLGNSCQHGCFNFDKNDSGNALNRIVAELPPRPA
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Best Local Similarity
Matches 191; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 777 amino acid
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/281902 FILING DATE: 28-JUL-1994
                                                                                                                                                                                                                                                                                            39 LGARYDAAQANLAFRYYSSRATRVEVFLYKNPTGSQEVARLALSKDPATQVWSLSLPTST 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
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QNDVDPNSTAGDNYWGYMTLNYFAPDRRYAYDKSAGGPTREWKAMVKAFHDAGIKVY IDV
                                    -NSVDETDPTQDN-WGYDPRNYDVPEGQYATNANGNARIKEFKEMVLSLHREHIGVNMDV 578
                                                                                                         DVRDFSIDPNSGMKNKGKYLALTEKGT-KGPDNVKTGIDSLKQLGITHVQLMPVFAS--- 520
                                                                                                                                                                                                                     IKNTYGITGAVYYGYRAWGPNWPYDAAWTKGSATGFVSDVDNAGNRFNPNKLLLDPYARE 158
                                                                                                                                                                                                                                                      LENW-----TRTAVDPYATA 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PDGAQADSAYFNGADNHALAWRIDGSEFGDSASAIYVAYNGWSGAVDFKLPWPGTGKQWY 733
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                                                                       HVR-----GLTRNDDSVPAAERGTYKGAARKAA---ALAALGVTAVEFLPVQETQND
                                                                                                                                              ISODPNTATCADGTIYATGAAHRNKDSGLCASKGIALAADATSVGSKPTRALKDEVIYEV 218
                                                                                                                                                                                  IAPNGTRGMIVD--LAKTDPAGWNSDKHI-----
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                                                                                                                                                                                                                                                                                                                                                                 10.1%; Score 509; DB 5; Length 777; 25.5%; Pred. No. 1.9e-31; tive 91; Mismatches 290; Indels 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCT/US95/09323
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RESULT 13
5457037-5
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PATCH NO. 5457037

APPLICANT: TOGNONI, ANGELO; CARRERA, PAOLO; CAMERINI, BARBARA;
GALLI, GIULIANO; LUCCHESE, GIUSEPPE; GRANDI, GUIDO; DI GENNARO, CARLK
TITLE OF INVENTION: CLONING OF THE GENE CODING THE ISOAMYLASE
ENZYME AND ITS USE IN THE PRODUCTION OF SAID ENZYME
NUMBER OF SEQUENCES: 7

CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                    Matches 184;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/1,
FILING DATE: 08-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 749,621
FILING DATE: 19-AUG-1991
APPLICATION NUMBER: 224,114
466 VRDFS-IDPNSGMKNKGKYLALTEKGTKGPDNVKTGIDSLKQLGITHVQLMPV----FA
                                                                                                                                                             400
                                                                                                                                                                                                                         344 IGNTY--TOKATTEKVWAPTSTOVNVLLYDSATG-SVTKIVPMTASGHGVWEATVNONL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           917
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                                                                                                                           89
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                                                    SQDPLNPSNQNGNVFASGASYRTTDSGIYAPKGVVLVPSTQSTGTKPTRAQKDDVIYEVH 186
                                                                                                                         KAAGITGAVYYGYRAWGPNWPYASN-WGKGSQAGFVSDVDANGDRFNPNKLLLDPYAQEV 126
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                                                                                      A-----PNGTRGMIVDLA---KTDPAGWNSDKHIT------PKNIEDEVIYEMD 465
                                                                                                                                                                                            LGASYDAQQANITFRYYSSQATRIVLYLYSAGYGVQESATYTLSPAGSGVWAYTVPVSSI 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NATSGKVGESTLGQAEGSVQVPGISMMI 944
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Pred. No. 9.7e-30;
95; Mismatches 271;
                                                                                                                                                           -----TRTAVDPYATAI 425
                                                                                                                                                                                                                                                                                              Length 751;
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RESULT 14
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; APPLICANT: TOGNONI, ANGELO:CARRERA, PAOLO:CAMERINI, BARBARA; GALLI, GIULIANO:LUCCHESE, GIUSEPPE:GRANDI, GUIDO:DI GENVARO, CARLC; TITLE OF INVENTION: CLONING OF THE GENE CODING THE ISOAMYLASE; ENZYME AND ITS USE IN THE PRODUCTION OF SAID ENZYME; NUMBER OF SEQUENCES: 7
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Best Local Similarity
                                                                                                                                                                                                                                                                             Matches
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FILING DATE: 08-JAN-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
    466
                                          126
                                                                                                                                                            400
                                                                                                                                                                                                                      344 LGNTY--TQKATTFKVWAPTSTQVNVLLYDSATG-SVTKIVPMTASGHGVWEATVNQNL-
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                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 749,621
FILING DATE: 19-AUG-1991
APPLICATION NUMBER: 224,114
FILING DATE: 25-JUL-1988
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                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 750
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VRDFS-IDPNSGMKNKGKYLALTEKGTKGPDNVKTGIDSLKQLGITHVQLMPV----FA
                                      SQDPLNPSNQNGNVFASGASYRTTDSGIYAPKGVVLVPSTQSTGTKPTRAQKDDVIYEVH 185
                                                                              A----PNGTRGMIVDLA---KTDPAGWNSDKHIT------PKNIEDEVIYEMD 465
                                                                                                                    KAAGITGAVYYGYRAWGPNWPYASN-WGKGSQAGFVSDVDANGDRFNPNKLLLDPYAQEV 125
                                                                                                                                                                                              LGASYDAQQANITFRVYSSQATRIVLYLYSAGYGVQESATYTLSPAGSGVWAVTVPVSSI 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YNH-----TFATQISDFDKIVPEYYYRTMIQVIIPTDQVLEMKLXAERPMVQK 627
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QGGDEYLRTLQCNNNAYNLDSSANWLTYSWTTDQSNFYTFAQRLIAFRKAHPALRPSSWY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ILREFTVRPAAGGSGLDLFAEPWAIGGNSY - - - - QLGGFPQGWSEWNG - - LFRDSLR - - -
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                                                                                                                                                                                                                                                                               183;
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                                                                                                                                                                                                                                                                                             9.5%;
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                                                                                                                                                                                                                                                                       Score 482; DB 6; I
Pred. No. 2.4e-29;
86; Mismatches 271;
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RESULT 15
US-09-129-075-4
US-09-129-075-4
; Sequence 4, Application US/09129075
; Patent No. 6087149
; Patent No. 6087149
; Patent No. 60871491
; APPLICANT: Tsutsum1, No. 60871491ko
APPLICANT: Bisgard-Frantzen, Henrik
APPLICANT: Svendsen, Allan
: TITLE OF INVENTION: Starch Conversion Proces
; FILE REFERENCE: 5262.204-US
; CURRENT APPLICATION NUMBER: US/09/129,075
; CURRENT FILING DATE: 1998-08-04
; EARLIER APPLICATION NUMBER: 60/055,867
; EARLIER APPLICATION NUMBER: 60/055,867
; EARLIER APPLICATION NUMBER: 60/055,867
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                                                                                                                        Ouery Match 9.4%; Score 475; DB 3; Length 726; Best Local Similarity 26.8%; Pred. No. 8e-29; Matches 166; Conservative 88; Mismatches 211; Indels 1
                                                                                                                                                                                                                                                                           SEQ ID NO 4
LENGTH: 726
                                                                                                                                                                                                                  LENGTH: 726
TYPE: PRT
ORGANISM: Rhodothermus marinus
-09-129-075-4
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EARLIER FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                        LGNTYTQKATTFKVWAPTSTQVNVLLYDSATG-SVTKIVPMTASGHGVWEATVNQNLENW
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                                                    LGATWDGLGVNFALYSQHAEAVELVLFDHPDDPAPSRTIEVTERTGPIWHVYLPGLRPGQ
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574 -LEFVRQTIWFRKQHRSFR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82
                                                                                           ---LAQAVVMT----SQGVPFMQGGEEMLRXKGGNDNSYNAGDAVNEFDW----SRKAQYPD 838
                                                                                                                                            PFASINEVTAHDGFTLEDLVSYTKKHNEANLEGNRDGMDENYSTNCGVEGPTQDPSVLAC 515
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                                   VFNYYSGLIHLRLDHPAFR
                                                                       REALKRSLISTLFLSQGVPMLLGGDELSRTQHGNNNAYCQDNEISWYNWQLDTRKQQF-- 573
                                                                                                                                                                                                                       QVGHFPWQWTEWNGRYRDAV------RFFWRGDRGLNGEFATRFAGSSDLYERSGRR 455
                                                                                                                                                                                                                                                           QKG---MGVAVENDNLRNALDGNVFDSSAQGFATGATGLTDAIKNGVEGSINDFTSS--- 750
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-09-802-640-32
-09-739-449-8719

Sequence 2. Application US/09262126C GENERAL INFORMATION: APPLICANT: Miller, Brian S. APPLICANT: Shetty, Jayarama K. TITLE OF INVENTION: Modified Forms of Pullulanase FILE REFERENCE: GC396-2 CURRENT APPLICATION NUMBER: US/09/262,126C CURRENT FILING DATE: 1999-03-03 NUMBER OF SEQ ID NOS: 9 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 2 LENGTH: 956 TYPE: PRT ORGANISM: Bacillus deramificans FEATURE: NAME/KEY: VARIANT ICCATION: (1)...(956) CTHER INFORMATION: Xaa - Any Amino Acid US-09-262-126C-2 RESULT 1 US-09-262-126C-2

7	Query Match Best Local Matches 95	Query Match 99.9%; Score 5054; DB 5; Length 956; Best Local Similarity 100.0%; Pred. No. 0; Matches 956; Conservative 0; Mismatches 0; Indels 0; Gaps	w
δ	1	MAKKLIYVCLSVCLVLTWAFNVKGQSAHADGNTTTIIVHYFCCPAGDYQPWSLWMWPKDGG 60	_
В	1	MAKKLIYVCLSVCLVLTWAFNVKGQSAHADGNTTTIIVHYFCPAGDYQPWSLWMWPKDGG 60	0
Ş	61		120
Дb	61	GAEYDFNQPADSFGAVASADIPGNPSQVGIIVRTQDWTKDVSADRYIDLSKGNEVWLVEG 120	õ
΄δ	121		ŏ
В	121	NSQIFYNEKDAEDAAKPAVSNAYLDASNQVLVKLSQPLTLGEGXSGFTVHDDTANKDIPV 180	ŏ
γQ	181		ö
밁	181	TSVKDASLGQDVTAVLAGTFQHIFGGSDWAPDNHSTLLKKVTNNLYQFSGDLPEGNYQYK 2	240
Ϋ́	241	VALNOSWNNSYPSDNINLTVPAGGAHVTFSYIPSTHAVYDTINNPNADLQVESGVKTDLV 300	ŏ
В	241	VALNDSWNNSYPSDNINLTVPAGGAHVTFSYIPSTHAVYDTINNPNADLQVESGVKTDLV 300	ŏ
Ϋ́	301	TVTLGEDPDVSHTLSIQTDGYQAKQVIPRNVLNSSQYYYSGDDLGNTYTQKATTFKVWAP 360	õ
日	301	TVTLGEDPDVSHTLSIQTDGYQAKQVIPRNVLNSSQYYYSGDDLGNTYTQKATTFKVWAP 360	õ

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Sequence 3, Application US/09262126C
GENERAL INFORMATION:
APPLICANT: Miller, Brian S.
APPLICANT: Shetty, Jayarama K.
TITLE OF INVENTION: Modified Forms of Pullula
FILE REFERENCE: GC396-2
CURRENT APPLICATION NUMBER: US/09/262,126C
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 718
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                                                                                                                                                 ; TYPE: PRT; ORGANISM: Bacillus subtilis US-09-262-126C-3
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                                                                                           Conservative
                                                                                        20.5%; Score 1039.5;
34.3%; Pred. No. 8.6
Live 125; Mismatches
-QIGAVI-RTAAFDDEFYYDG-ELGAVYTADHT
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                                                                                        .5; DB 5;
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les 272;
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; TYPE: PRT
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                                                                                                              Matches
                                                                                                                           Query Match
Best Local Similarity
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CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Miller, Brian S.
APPLICANT: Shetty, Jayarama K.
TITLE OF INVENTION: Modified Forms of Pullulanase
FILE REFERENCE: GC396-2
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AVASADIPGNPSQVGIIVRTQDWTKDVS-----ADRYIDLSKGNEVWLVEGNSQIFYNEK 129
                                    VPGEAVTAVENQA--VIHLVDIAGITSSSAADYSSKNLYLWN-----NETCDALS
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                                IIVVYNPNKTVATINLPSGK-WAINATSGKVGESTLGQ-----AEGSVQVPGISMMIL 945
                                                                                                                                                                                  DNSYNAGDAVNEFDWS------
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                                                                                                         YSGLIHLRLDHPAFRMTTANEINSHLQFLNSPENTVAYELTDHVN-----KDKWGN 893
                                                                                                                                                                                                                                                         YVTSHDNYTLWDKIALSNPNDSE-ADRIKMDELAQAVVMTSQGVPFMQGGEEMLRXKGGN 815
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LVVAINAAPESRTLNEFAGETLQLSAIQQTAGENSLANGVQIAADGTVTLPAWSVAVL
                                                                      YQELTELRKSSPLFTLGDGSAVMKRVDFRNTGSDQQAGLLVMTVDDGMKAGASLDSRLDG
                                                                                                                                             RDSYDSGDWFNRVDYSLQDNNYNVGMPRISDDGSNYEVITRVKEMVATPGEAELKQMTAF 956
                                                                                                                                                                                                                    YVSKHDNQTLWDMISYKASQEADLATRVRMQAVSLATVMLGQGIAFDQQGSELLRSKSFT
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RESULT

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; SOFTWARE: PatentIn Ver. 2.0; SEQ ID NO 5; LENGTH: 793; TYDE: PRT; ORGANISM: Solanum tuberosum US-09-463-238-5
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APPLICANT: Martin, Catherine R
APPLICANT: Plant Bioscience Limited
TITLE OF INVENTION: Starch Debranching Enzymes
FILE REFERENCE: 97.118
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CURRENT FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: PCT/GB98/02280
PRIOR FILING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: GB 9716185.5
PRIOR FILING DATE: 1997-07-31
NUMBER OF SEQ ID NOS: 30
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                                             RKAQYPDVFNYYSGLI------HLRLDHPAFRMTTANEINSHLQFLNSPE-----NTV 878
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KKDESSSDFLRFCGLMTKFRHECESLGLD----GFPTAERLQWHGHTPRTPDWSETSRFV
                                                                                                                                                                                             PNLYQKGGRKPWNSINFYCAHDGFTLADLYTYNNKHNLANGEDNKDGENHNNSWNCGEEG
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                                                                                             EFASIFVKKLRKRQMRNFFLCLMVSQGVPMIYMGDEYGHTKGGNNNTYCHDNYINYFRWD
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CURRENT APPLICATION NUMBER: US/09/463,238
CURRENT FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: PCT/GB98/02280
PRIOR FILING DATE: 1998-07-30
PRIOR PRICATION NUMBER: GB 9716185.5
PRIOR FILING DATE: 1997-07-31
NUMBER OF SEQ ID NOS: 30
SOFTMARE: PALENTIN Ver. 2.0
SEQ ID NO 6
LENGTH: 766
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APPLICANT: Smith, Alison M
APPLICANT: Bustos Guillen, Regla
APPLICANT: Bustos Guillen, Regla
APPLICANT: Martin, Catherine R
APPLICANT: Plant Bioscience Limited
TITLE OF INVENTION: Starch Debranching Enzymes
FILE REFERENCE: 97.118
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FMQGGEEMLRXKGGNDNSYNAGDAVNEFDWSR-KAQYPDVFNYYSGLIHLRLDHPAFRMT 859
                                                                                                                                                                                            NALDGNVFDSSAQG-FATGATGLTDAIKNGVEGSINDFTSSPGETINYVTSHDNYTLWDK 769
                                                                 VSYNNKHNDANGEGGNDGCNDNFSWNCGIEGETSDANI NALRSRQMKNFHLALMVSQGTP
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                                                                                                             -----RIKMDELAQAVVMTSQGVP 800
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PRIOR APPLICATION NUMBER: PCT/G598/02280
PRIOR FILING DATE: 1998-07-30
PRIOR FILING DATE: 1997-07-31
PRIOR FILING DATE: 1997-07-31
NUMBER OF SEQ ID NOS: 30
SOFTMARE: Patentin Ver. 2.0
SEQ ID NO 14
PRIOR TERM
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; LCCATION: (274, 276)
; OTHER INFORMATION: Xaa - unknown amino
US-09-463-238-14
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APPLICANT: Martin, Catherine R
APPLICANT: Plant Bioscience Linited
TITLE OF INVENTION: Starch Debranching Enzymes
FILE REFERENCE: 97.118
CURRENT APPLICATION NUMBER: US/09/463,238
CURRENT FILING DATE: 2000-01-21
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APPLICANT: Smith, Alison M
APPLICANT: Bustos Guillen, Regl
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                                                                                                                                                                                                                                                                                                                              541 DVPEGQYATNANGN---ARIKEFKEMVLSLHREHIGVNMDVVYNHTFATQ----ISDFDK 593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 FYOGKPLPFGATATDGGVNFAVFOGNATAATLCLITLSDLPEKRVTEQIFLDPLANKTGD 181
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AEAWDCGGLYQVGMFPHWGIWSEWNGKYRDMV---
                                                                                                                                    LMALLGKDTMSKAASELHAINP-GIALYGEPWTGGT----SALPDDQLLTKGA---
                                                                                                                                                                                                                                 IVPEYYYRTMIQVIIPTDQVLEMK-----LXAERPMVQKFIIDSLKYWVNEYHIDGFRFD 648
                                                                                                                                                                                                                                                                                FSPMGRYSSAGLSNCGLGAINEFKYLVKEAHKRGIEVIMDVVFNHTAEGNENGPILSFRG
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                                                                                        LASIL----TRSSSSWNAVNVYGNSIDGDVITTGTPLTSPPLIDMISNDPIL-RGVKLI
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                                            -QKGM----GV-AVFNDNLRNALDGNVFDSSAQGFATGATGLTDAIKNGVE 741
-----RQFIKGTDGFSGAFAECLC
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US-09-463-238-15
; Sequence 15, Application US/09463238
; GENERAL INFORMATION:
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; TYPE: PRT
; ORGANIZM: Solanum tuberosum
US-09-463-238-15
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SEQ ID NO 15
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CURRENT FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: PCT/GB98/02280
PRIOR FILING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: GB 9716185.5
PRIOR FILING DATE: 1997-07-31
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APPLICANT: Martin, Catherine R
APPLICANT: Plant Bioscience Inited
TITLE OF INVENTION: Starch Debranching Enzymes
FILE REFERENCE: 97.118
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APPLICANT: Smith, Alison M
APPLICANT: Bustos Guillen, Regl
APPLICANT: Martin, Catherine R
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935 VQVPGISMMILHQEVSP
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                                                                                                                                                                                                                                            NDNFSWNCGIEGETSDANINALRSROMKNFHLALMYSQGTPMMLMGDEYGHTRYGNNNSY
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                                                               SRELAFMLHD----GNGGDIYLAFNAHHFSIKTAIPSP--PRNRSWYRVVDTNLKSPDDF
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Best Local Similarity
Matches 148; Conserv
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SEQ ID NO 4
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PRIOR FILING DATE: 1997-07-31
NUMBER OF SEQ ID NOS: 30
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APPLICANT:
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CURRENT FILING DATE: 2000-01-21
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TYPE: PRT
ORGANISM: Solanum tuberosum
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                                                        751 PGETINYVTSHDNYTLWDKIAL-SNPNDSEAD------RIKMDELAQAV
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                                                                                                                                                                                                                                                                                                                                                                                                                      534 G-YDPRNYDVPEGQYATNANGNARIKEFKEMVLSLHREHIGVNMDVVYNHTF----ATQI 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     371 KLPDDLAGTFSGISEKW-------HHFKDLGVNAMLLEPIF------PFDEQK 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     172 VELDFEASLAPFYISFYMKSQLVSDMENS-----EIRSHRNTNFVVPVGLSSGHPAPLGI 226
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              PAFSFNYIARNSGLTLVDLVSFSSNEVASELSWNCGQEGATTNNIVLERRLKQVRNFLFI 676
                                                                                                       WNPLTNDSKENLFPHWRRWAEINMRFCDDIRDFLRG·EGLLSNLATRLCGSGDIFAGGRG
                                                                                                                                                  ---LRNALDGNVFD-------SSAQGFATGATGLTDAIKNGVEGSINDFTS--S
                                                                                                                                                                                            -----VNASSLLRGFN-GEILSRPPL---VEAIAFDPILSK-----VKMIADN
                                                                                                                                                                                                                                       LMALLGKDTMSKAASELHAINPGIALYGEPWTGGTSALPDDQLLTKGAQKGWGVAVFNDN 708
                                                                                                                                                                                                                                                                                                                              SDFDKIVPEYYYRTMIQVIIPTDQVLEMKLXAERPMVQKFIIDSLKYWVNEYHIDGFRFD 648
                                                                                                                                                                                                                                                                                                                                                                             GPYFPWHFFSPGNMYGPSGDPLSAIKSMKDMVKKLHANGIEVFLEVVFTHTAEDAPLMNV
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Martin, Catherine R
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Gaps

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TITLE OF INVENTION: Starch Debranching Enzymes
FILE REFERENCE: 97.118
CURRENT APPLICATION NUMBER: US/09/463,238
CURRENT FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: PCT/GB98/02280
PRIOR FILING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: GB 9716185.5
PRIOR APPLICATION NUMBER: GB 9716185.5
PRIOR FILING DATE: 1997-07-31
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 19
LENGTH: 883
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GENERAL INFORMATION:
APPLICANT: Edwards, Elizabeth A
APPLICANT: Smith, Alison M
APPLICANT: Bustos Guillen, Regla
APPLICANT: Martin, Catherine R
APPLICANT: Plant Bioscience Limited
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 5.3%;
Best Local Similarity 22.4%;
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649 LMALLGKDTMSKAASELHAINÞGIALYGEPWTGGTSALÞDDQLLTKGAQKGMGVAVFNDN |: |: | : |: | : | : | : |
                                                   476 DNFSYCIKGGQYLN-----IQNALNCNYPIVQQMILDCLRHWVIEFHIDGFVF-
                                                                        589 SDFDKIVPEYYYRTMIQVIIPTDQVLEMKLXAERPMVQKFIIDSLKYWVNEYHIDGFRFD
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                                                                                                                        GPYFPWHFFSPGNMYGPSGDPLSAIKSMKDMVKKLHANGIEVFLEVVFTHTAEDAPLMNV
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18; Pred. No. 8.2e-12;
91; Mismatches 258;
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; Sequence 8397, Application US/09739449
; GENERAL INFORMATION:
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PRIOR FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 13351
SEQ ID NO 8397
LENGTH: 379
TYPE: PRT
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Query Match 5.2%; Score 265; DB 5; Best Local Similarity 23.1%; Pred. No. 4.4e-12; Matches 97; Conservative 71; Mismatches 148
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APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15490)C
CURRENT APPLICATION NUMBER: US/09/739,449
CURRENT FILING DATE: 2000-12-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              613 VLEMKLXAERPMVQKFIIDSLKYWVNEYHIDGFRFDLMALLGK-----DTMSKAASELHA 667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         504 LKQLGITHVQLMPVFASNSVDETD----PTQDNWGYDPRNYDVPEGQYATNANGNARIKE 559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTGNTVACDHPYIRQLIVDSLRHFVLNAGVDGFRFDLAPVLGRTAAGFDMASETLAAMHS
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                                                                         DVFNYYSGLIHLRLDHPAFRMTTANE INSHLQFLNSPENTVAYELTDHVNKDKWGNIIVV
                                                                                                                                                                                                                       EADRIKMDELAQAVVMTSQGVPFMQGGEEMLRXKGGNDN-SYNAGDAVNEFDWSRKAQYP
                                                                                                                                                                                                                                                                                                       -RRFWRGDAGTTGALANALSGSSPIFSRHGRLKSRSVNFLAAHDGFTLFDLVSHERKHNE
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--FEGL----TDDPAIVAARLADVKALLSTLFVSRGTLMLTAGDEGGRSQQGNTMPI
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CURRENT APPLICATION NUMBER: US/08/945,567C
CURRENT FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 08/41,718
PRIOR FILING DATE: 1995-05-01
PRIOR APPLICATION NUMBER: 08/478,370
PRIOR APPLICATION NUMBER: 08/621,944
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 08/621,944
PRIOR FILING DATE: 1996-03-26
PRIOR APPLICATION NUMBER: PCT/CA96/00264
PRIOR FILING DATE: 1996-04-29
NUMBER OF SEC ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
SED ID NO 4
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; TYPE: PRT
; ORGANISM: MORAXELLA CATARTHALIS
US-08-945-567C-4
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APPLICANT: HARKNESS, Robin E.
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: CHONG, Pele
APPLICANT: CHONG, Pele
TITLE OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE PROTEIN OF
TITLE OF INVENTION: MORAKELLA
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                                           495 DNVKTGIDSLKQLGITHVQLMPVFASNSVDETDPTQDNWGYDPRNYDVPEGQYATNANG- 553
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                                                                                           NGLNIKTDKNGTV-----TFGINTTSGLKAGKSTLNDG---GLSIKNPTGS
                                                                                                                                         AGWN--SDKHITPKNIEDEVIYEMDVRDFSIDPNSGMK-----NKGKYLALTEKGTKGP 494
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ū 45;	/ Match 3.9%; Score 196; DB 4; Length 1992; Local Similarity 19.1%; Pred. No. 3.5e-06; nes 197; Conservative 141; Mismatches 377; Indels 318; Gaps	Query Ma Best Loo Matches	
	TYPE: PRT ORGANISM: Moraxella catarrhalis 8-945-567C-3	TYPE: ORGAN S-08-945	g ·· ··
	NO 3 H: 1992	SEQ ID NO	٠. ٠.
	RE: Patentin Ver. 2.1	SOFTWARE:	٠
	NG DATE: 1996-04-29	PRIOR I	
	ETLING DATE: 1996-03-26 APPLICATION NUMBER: PCT/CA96/00264	PRIOR I	·· ··
	APPLICATION NUMBER: 08/621,944		٠
	APPLICATION NUMBER: 08/478,370	PRIOR	
	PRIOR APPLICATION NUMBER: 08/431,718 PRIOR FILING DATE: 1995-05-01	PRIOR I	٠. ٠.
	T FILING DATE: 1998-03-19	CURREN	٠
	T ADDITION NUMBER: 118/09/945 5670	FILE R	
N OF	OF INVENTION: HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE PROTEIN OF INVENTION: MORAXELLA	TITLE	
		APPLICANT:	
	CHONG, Pele	APPLICANT:	.,
		APPLICANT:	
	CASAKT KAN	GENERAL.	
	2 -567C-3 e 3, Application US/08945567C	RESULT 12 US-08-945-5 ; Sequence	·· 2
	NKEQVNDANKKQG 1247	b 1235	g
	GKWAINATSGKVG 924	y 912	Qy
1234	YVDADGNKVIYDSTDNKYYQAKNDGTVDKTKEVAKDKLVAQAQTPDGTLAQMNVKSVI 12	b 1177	망
911	LNSPENTVAYELTDHVNKDKWGNIIVVYNPNKTVATINLPS	y 870	γQ
1176	LGVKTTTLTSTGTGANKFALSNQATGDALVKASDIVAHLNTLSGDIQTAKGASQANNSAG 11	b 1117	DЬ
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1116	DFVSTYDTVNFADGNAITAKVTYDDTSKTSKVVYDVNVDDTTIEVKDKK 11	b 1068	рь
613	YVTSHDNYTLWDKIALSNPNDSEADRIKWDELAQAVVMTSQGVPFMQGGEEMLRXKG	y 756	γo
1067	LSNTLANVTNDKGSVRTTEQGNIKDEDKTRAASIVDVLSAGFNLQGNGEAV 10	0 1016	망
55	NDFTSSPGETI 7	y 716	Qγ
1015	NGITTKVNKGVVRVGIDQTKGLTTPKLTVGNNNGKGIVIDSQNGQNTITG 10	966	ДD
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US-09-739-449-12578
Sequence 12578, Application US/09739449
GENERAL INFORMATION:
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; TYPE: PRT ; ORGANISM: Agrobacterium tumefaciens US-09-739-449-12578
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APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences
FILE REFERENCE: 38-10(15490)C
CURRENT EILING DATE: US/09/739,449
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 09/514,000
PRIOR FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 13351
SEQ ID NO 12578
LERGTH: 530
TYPE: DEF
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens
FILE REFERENCE: 38-10(15490)C
CURRENT APPLICATION NUMBER: US/09/739,449
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 09/514,000
PRIOR FILING DATE: 2000-02-23
                                                                                                                                                                          Sequence 9531, Application US/09739449 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            471
                                                                                                                                                                                                                                                                                                                404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       674 LYGEPWTGGTSALPDD-----QLLTKGAQKGMGVAVFND------NLRNALDGNVFDSS 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93 --- GWGYDGVLQFSPQRDYGTPD-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FDGLRIDAADHLAGGDGEVDFLIEMAREVKRTIRNRHVHLVIEDARNAASPMTPMADGAI 246
                                                                                                                                                                                                                                                                                                              PPDASQ------MVMDPNDQ-HTMQLSTLKWTHAETTEGR 436
                                                                                                                                                                                                                                                                                                                                                                                             NPNDSEADRIKMDEL-----AQAVVMTSQGVPFMQGGEEMLRXKGGNDNSYNAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LVDAQWN-----DDFHHVIHVATTNEEGG----IYEDFASRPYENLRRSL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IDPNSGMKNKGKYLALTEKGTKGPDNVKTGIDSLKQLGITHVQLMPV--FASNSVDETDP 528
                                                                                                                                                                                                                                                                                                                                                    TDHVNKDKWGNIIVVYNPNKTVATINLPSGKWA-INATSGK 922
                                                                                                                                                                                                                                                                                                                                                                                                                                        DAVNEFDWSRKAQYPDVFNYYSGLTHLRLDHPAFRMTTANEINSHLQFLNSPENTVAYEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---DQAGNRLRGERLRALIPPPLFGTLEAILLLCPQTPLVFMGDE-----HGSANP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----ATGF---VYQGEPRPSRNFAASGEPSGHLPPHRFVNFLHNH------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQGFATGATGLTDAIKNGVEGSINDFTSS-----PGETINYVTSHDNYTLWDKIALS 773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IDGFRFDL-----SKAASELHAINPGIA 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RTRVADPASNRQQEGPRGPSLIVNHDFAWKNP-NWKG-----RPWHEAVVYELHIGTFT
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                                                                                                               Genome
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                                                                                                                                                                                                                                                    RESULT 15
US-09-739-449-9662
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         APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15490)C
CURRENT APPLICATION NUMBER: US/09/739,449
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 09/514,000
PRIOR FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 13351
SEQ ID NO 9662
LENGTH: 533
                                                                                                                                                                                                              Sequence 9662, Application US/09739449 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 115; Conserv
TYPE: PRI
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                                                                                                                                                                                                                                                                                                                                                TLGQAEG-SVQVP 938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----ELRD-NPALA----PERRNASTAPAVNPYNFQEHLYDKNRPENI---AFLKRFRAV 248
                                                                                                                                                                                                                                                                                                                                                                                                                                  QFLNSPENTVAYELTDHVNKDKWGN--IIVVYNPNKTVATINLPSGKWAINATSGKVGES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLMTQRGSVCIYEGEELGLTEADIAFEDLQDPYGIQFWPEFKGRDGCRTPMVWDAGHAQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LDEFPDIAAVGEVGDS-------QRGLE-IVGEYTSGDDKMQMCYAFEFLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LD------GNVFDSSAQGFATGATGLTDAIKNGVEGSINDFTS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KAASELHAINPGIALYGEPWTGGTSALP-----DDQLLTKGAQKGMGVAVFNDNLRNA 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MHNFL-----TSQPDLNLHNPEVQEELLNITRFWLKR-GVDGFRLDTINFYFHDL--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.2%; Score 161.5; DB 5; Length 532; ilarity 18.8%; Pred. No. 0.00013; Conservative 75; Mismatches 198; Indels 225;
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; ORGANISM: Agrobacterium tumefaciens
US-09-739-449-9662
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                                                                                                                                                                                                                                                                                                                                                                                                                              600 YRTMIQVIIPTDQVLEMKLXAERPMYQKFIIDSLKYWVNEYHIDGFRFDLM------
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417 LPVPYVHAMQAVDAQERKPDSVLNHYRAVLSFRKTHGALRDGDMHFIKTNLDVL
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                                                                              CLYQGEELGLTEAELAFEDLRDPYGIRFWPAFKGRDGCRTPMVWETGKPNAGFSTAEKPW
                                                                                                                                                                                   FTSSPGETINYVTSHDNYTLW-----DKIA-LSNPNDSEADRIKMDELAQAVVMTSQGVP 800
                                                                                                                                                                                                                                        RALLDDYEGRATYGEVGDGARSLKTVAAYTSGNDKLNMCYTFDLLGPDFSAKHLRGSVET 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPMAD-----MGYDVSDYCNVDPMFGT-----LADFDALMAEAHRLGLKVIIDQV
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                                                                                                                    FMQGGEEM------LRXKGG------
                                                                                                                                                          F----GKVVT-----DGWVCWAFSNHDVVRHLSRFSEGPEEQTRVAKLAICVLASLRGSI
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                -SRKAQYPD-VFNYYSGLIHLRLDHPAFRMTTANEINSHLQFL:: | | | | : | : | | | : | : | |
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Search completed: April 22, 2001, 09:09:21 Job time: 697 sec

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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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isoamylase (EC 3.2
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A;Status: preliminary A;Molecule type: DNA A;Residues: 1-843 <ARN>

GB:AE000512; NID:g4982421; PIDN:AAD36907.1; PID:g498

A; Title: Evidence for lateral gene transfer A; Reference number: A72200; MUID:99287316 A; Accession: H72204

between Archaea and

Bacteria

from

genome

Hic

Nature 399, 323-329, 1999

ALIGNMENTS

pullulanase - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Species: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Ju1-2000
C;Accession: H72204

R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hi Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,

Ş Вb Ş 밁 Ş 밁 Ş 밁 밁 Ş á 맑 Ş A;Cross-references: GB:AE001821; G A;Experimental source: strain MSB8 C;Genetics: A;Gene: TM1845 Query Match Best Local S Matches 349 379 174 140 190 259 199 143 90 91 21 Local Similarity mes 349; Conserv 34 TTIIVHYFCPAGDYQPWSLWMWPKD---GGGAEYDFNQPADSFGAVASADIPGNPSQVGI 90 TVPAGGAHVTFSYIPSTHAVYDTINNPNADLQVESGVKTDLVTVTLGEDPDVSHTLSIQT TFQHIFGGSDWAPDNHSTLLKKVTNNLYQFSGDLPEGNYQYKVALNDSWNNSYPSDNINL FLTNPVDTKKKELFKVT------ 173 EGYKPARVIMMEILD--DYYYDG-ELGAVYSPEKTIFRVWSPVSKWVKVLLFKNGEDTEP Conservative 31.0%; Score 1570; DB 2; 36.6%; Pred. No. 6.9e-82; tive 145; Mismatches 291 -----DIDVTNY-VRIVLSESL------291; Length 843 Indels Gaps 189 258 259 318 22

BVECGX C83375

glycogen probable

operon pr alpha-glu glycosyl

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A;Ktetus: preliminary
A;Kolecule type: DNA
A;Kolecule type: DNA
A;Residues: 1-717 <5TO>
A;Cross-references: GB:AP001518; GB:BA000004; NID:g10175792; PIDN:BAB06983.1; GSPDB:GN00
A;Cross-references: GB:AP001518; GB:BA0000004; NID:g10175792; PIDN:BAB06983.1; GSPDB:GN00
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A;Tille: Complete genome sequence of the alkaliphilic bacterium Bacillus halodur A;Reference number: A83650; MUID:20263314
A;Accession: H84057
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                                                                                                                                                                     QYVYNG-ELGALYSHERTVFAVWTPVATEVSLLLYENWHTLEAIEYQMKRSPNGVWSVSL 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IDPTI1LYGEPWGGWGAPI----RFGKSDVAGTHVAAFNDEFRDAIRGSVFNPSVKGFVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YLNESGCGNVIASERPMMRKFIVDTVTYWVKEYHIDGFRFDQMGLIDKKTMLEVERALHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HTRIREVKEMVKALHKHGIGVIMDMVFPHTYGIGELSAFDQTVPYYFYR----IDKTGA
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                                                                                                                                                                                                                                                        Conservative 118;
                                                                                                                                                                                                                                                    21.4%; Score 1084.5; DB 2; 37.5%; Pred. No. 2.8e-54; tive 118; Mismatches 255;
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697 FNGHTVSVQSRSSMVLYR
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                                                                                                                                                                                  GGNDNSYNAGDAVNEFDWSRKAQYPDVFNYYSGL1HLRLDHPAFRMTTANEINSHLQFLN
                                                                                                                                                                                                                                                              ETINYVTSHDNYTLWDKIALSNPNDSEADRIKMDELAQAVVMTSQGVPFMQGGEEMLRXK
                                                                              TPSEVIGFHY-HHIAKWGPWDEMVVLHNGGGDKVDIRLPASGEWEVIVDGKKAGLVPLYT
                                                                                                                  SPENTVAYELTDHVNK-DKWGNIIVVYNPNKTVATINLP-SGKWAINATSGKVGESTLGO
                                                                                                                                                            HGEGNSYNSPDWINQLDWSRRAIYAADVEYVKGLIALRKAHRAFCFSTFSEVNTHMCPLK
                                                                                                                                                                                                                                                                                                                         LAQARAVPFLHFFHDTFRDAVKGSTFDLNKGGFCAGNIELKETLIASMLGHEAQF-DRPS
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G65955

pullulanase amyX - Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: 65-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
C;Accession: G65965
C;Accession: G65965
R;Kunst, F; Ogasawara, N.; Moszer; I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber
C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
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Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal
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Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau
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Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanl
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sc
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T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Ittle: The complete genome sequence of the Gram-positive bacterium Bacillus subtili
A;Reference number: A69580; MUID:98044033
A;Cross-references: G8:Z99119; GB:AL009126; NID:92635411; PIDN:CAB14971.1; PID:el1858
A;Cross-references: G8:Z99119; GB:AL009126; NID:92635411; PIDN:CAB14971.1; PID:el1858
C;Genetics:
A;Gene: amyX

51;

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RESULT 4
A84112
alkaline amylopullulanase BH3697 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 *sequence_revision 01-Dec-2000 *text_change 31-Dec-2000
C;Accession: A84112
R;Takami, H; Nakasone, K; Takaki, Y.; Maemo, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20263314
A;Accession: A84112
A;Accession: A84112
A;Accession: A84112
                                                              A:Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1072 <STO>
A;Cross-references: GB:AP001519; GB:BA0000004; NID:g10176109;
A;Experimental source: strain C-125
C:Genetics:
A;Gene: BH3697
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    Similarity
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   Score
Pred.
 819; DB 2;
No. 7.5e-39;
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               Length 1072;
                                                                                                         PIDN:BAB07416.1;
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                                                                                                                                                                                                                                                                            LYGEPW-----TGGTSALPDDQLLTKGAQKGMGVAVFNDNLRNALDGNVFDSSAQGFAT
                                                                                                                                                                                                                                                                                                                                                                    ELRIKEFKHLIDEIHRRGMGVILDVVYNHTAAVEI--FEDLMPNYYH-FMDADGTPRTSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                 QNLENWYYMYEVTGQGSTRTAVDPYATAIAPNGTRG--MIVDLAKTDPAGWNSDKHITP-
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                            FLNSPE-----VNKDKWGN
                                                                                    DNSYNAGDAVNEEDWSR----KAQYPD----VFNYYSGLIHLRLDHPAFRMTTANEINSHLQ
                                                                                                                                       KMDELAQAVVMTSQGVPFMQGGEEMLRXK-----GGN------
                                                                                                                                                                                 GATGLTDAIKNGVEGSINDFT-SSPGETINYVTSHDNYTLWDKIALS---NPNDSEADRI 783
                                                                                                                                                                                                                                              MIGEGWRTYVGDEHGGDIMPADQ----DWMQHTESVGVFSDEFRNELKSGFGSEGQPRFIT
                                                                                                                                                                                                                                                                                                         GGGRLGTTHKMSRRILVDSITYWVEEYKVDGFREDMMGDHDAETIQIAYDRAKELNPNIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNLAGYYYHYKIERDGDTKLGLDPYAKSMAAWNNEGSYSIGKAAIVDPSSIGPELDFAEI
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LLDIPEISETDLVIGYRATSTDNTGTYYVFVNADTKERTLSLTDDLTEGVVIVDSDEAG-
                                                           HDSYDSSDAINKFDWGKATNKEKYPIHHLTRTYTAGLIELRRSTNAFTHGTLVDVQANVR
                                                                                                                       \tt KRIRLGNTMVLTAQGTAFLHAGQEFGRTKQFRADTGGQAPYKSTYMTDENGKPFVYPYFI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADLQVESGVKTDLVTVTLGEDPDVSHTLSIQTDGYQAKQVIPRN--VLNSSQYYYSGDDL
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RESULT 5

N75524

Alpha-delpha-glucosidase - Deinococcus radiodurans (strain R1)

C.Species: Deinococcus radiodurans

C.Species: Deinococcus radiodurans

C.Accession: D75524

R; White, O; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, S.; Smith, H.O.; Venter, J.C.; Frasor, C.M.

Science 286, 1571-1577, 1999
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A;Accession: D75524
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A;Experimental source: strain Ri
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A; Residues: 1-910 <WHI>
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Best Local Similarity
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393 AVNAVKDADAY -- NWGYDPYHSMVPEGSYAVNP -- AERTKEYRQMVMSLNAAGLRVVQDV 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HIFGGSDWAPDNHSTLLKKVTNNLYQFSGDLPEGNYQYKVALNDSWNNSYPSDNINLTVP 261
                                 ASNSVDETDPTQDNWGYDPRNYDVPEGQYATNANGNARIKEFKEMYLSLHREHIGVNMDV 578
                                                                       PGSDG----MTHLRALAGAGLKAVHLLPTFDIATINEDKGQWQTPGDLTQFGPNSEEQQK 392
                                                                                                             KGTKGPDNVKTGIDSLKQLGITHVQLMPVF-----
                                                                                                                                                     SVFADLSDNSQKPAGWNALKKPALRSFADLSFYELHLRDFSAADASVPAAERGTYLAFTR 336
                                                                                                                                                                                       GMIVDLAKTD--PAGWNSDKHITPKNIEDEVIYEMDVRDFS-IDPNSGMKNKGKYLALTE 488
                                                                                                                                                                                                                               ERTLPMTRDTQGVWTASGDQSWKGLAYRFEVRVFAPSTGNIETNLVTDPYSVALTRNSTH
                                                                                                                                                                                                                                                                   TKIVPMTASGHGVWEATVNQNLENWYYMYEV----TGQGSTRTAVDPYATAIAPNGTR 431
                                                                                                                                                                                                                                                                                                         ATCVQTAWAL-----DDLYAYAG-PLGVTWQGNKPTVRLWAPTAQDVK-LHVSRPDGTQ
                                                                                                                                                                                                                                                                                                                                             TDGYQAKQVIPRNVLNSSQYYYSGDDLGNTYTQKATTEKVWAPTSTQVNVLLYDSATGSV 377
                                                                                                                                                                                                                                                                                                                                                                                  ALQAKAPYL-----AGYKL------LQIRAADRAKLPTALSGQ-LAVSSVLPGGKVLD
                                                                                                                                                                                                                                                                                                                                                                                                                      AGGAHVTFSYIPSTHAVYDTINNPNADLQVESGVKTDLVTVTLGEDPDVSHTLS----IQ 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNOVLYKLSOPL----TLGEGXSGFTVHDDTANKDIPVTSVKDASLGODVTAVLAGTFO
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A;Title: Purification and molecular genetic characterization of ZPUl, a pullulanase-t A;Reference number: Z14395; MUID:99097061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        starch debranching enzyme, pullulanase-type - maize
C:Species: Zea mays (maize)
C:Date: 19-Feb-1999 *sequence_revision 19-Feb-1999 *text_change 29-Oct-1999
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A; Residues: 1-962 <BEA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: endosperm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:AF080567; NID:g3411265; PIDN:AAD11599.1; PID:g3411266
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Best Local Similarity
Matches 262; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                           Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genetics:
                     308
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                                                                                                                                                                                                                                                   134 AAKPAVSNAYLDASNQVLVKLSQPLTLGEGXSGFTVHDDTANKDIPVTSVKDASLGQDVT 19:
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PDVSHTLSIQTDGYQAKQVIPRNVLNSSQYYYSGDDLGNTYTQKATTFKVWAPTSTQVNV
                                                                                                                                                                       AVLAGTFOHIFGGSDW-APDNHSTLLKKVTNNLYQFSGDLPEGNYQYKVALNDSWNNSYP 252
                                                                                           SDNINLTVPAGGAHVT---FSYIPSTHAVYDTINNPNADLQVESGVKTDLVTVTL---GED
                                                                                                                                         SLIA----
                                                                                                                                                                                                               APRPPMATAEEGASSDVGV-----AVAESAQGFLL-------DARAYWVTK 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YNAGDAVNEFDWS------RKAQYPDVFNYYS
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                                                                                                                                                                                                                                                                                         15.8%; Score 797; DB 2; ilarity 27.0%; Pred. No. 1.1e-37; Conservative 143; Mismatches 325;
                                                       -VTOKEPEISS----YRAFRIPSS-VDVATLVKCQLAVASEDAHGNR 185
                                                                                                                                 -WNISDOKTSLFLYASRNATMCMSSODMKGYDSKVELQPE-NDGLP 142
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Gaps

37;

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alpha-dextrin endo-1,6-alpha-glucosidase (EC 3.2.1.41) - rice
N;Alternate names: pullulanase
C;Species: Oryza sativa (rice)
C;Date: 23-Apr-1999  #sequence_revision 23-Apr-1999  #text_change 21-Jul-2000
C;Accession: T03760
R;Nakamura, Y; Umemoto, T.; Ogata, N.; Kuboki, Y.; Yano, M.; Sasaki, T;
Planta 199, 209-218, 1996
.....s-rererences: EMBL:D50602; NID:g836661; PIDN:BAA09167.1; A;Experimental source: cv. Fujihikari, endosperm C;Genetics:
                                                                              A; Reference number: Z15063; MUID: A; Accession: T03760
A; Status: preliminary; translated
                                   A; Molecule type: mRNA
A; Residues: 1-986 <NAK>
A; Cross-references: EMB
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A:Reference number: 215063;
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C; Keywords: glycosidase; hydrolase; polysaccharide degradation
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Best Local Similarity 27.6%;
Matches 251; Conservative 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                LYGEGWDFGEVAQNKRGINASQI----NMSGTGIGSFNDRIRDSVNGGNPFGNPLQQGFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RPMVQKFIIDSLKYWVNEYHIDGFRFDLMALLGKDTMSKAAS-----ELHAI-NPGIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALNRIGLRVVMDVVYNHLDSSGPFGVSSVLDKIVPGYYLRRNVNGQIENSAAMN-NTASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DMFAYTG-PLGAVFSDKDVDLYLWAPTAQDVRVCFYDGPAGPLLQTVQLKEL-NGVWSVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VYDTINNPNADLQVESGVKTDLVTVTL---GEDPDVSHTLSIQTDGYQAKQVIPRNVLNS
                                                                  GQAEGSVQVP
                                                                                               AQNEKCKMAQLDKNFSYVVTIFNVCPHEVSIEIHDLASLGLELHPIQVNSSDALVRQSAY
                                                                                                                                HVNK------DK-WGNIIVVYN--PNKT-----VATINLPSGKWAINATSGKVGESTL
                                                                                                                                                                  FRPLKNHILSCFDNFVDILKIRYSSPLFRLSTASDIEQRVRFHNTGPSMVPGVIVMSIKD
                                                                                                                                                                                                ----KAQYPDVFNYYSGLIHLRLDHPAFRMTTANEINSHLQFLNSPEN----TVAYELTD
                                                                                                                                                                                                                                 FFHAGDEILRSKSLDRDSYNSGDWFKKLDLHMNQPIGCRLLQEIRMKNMHLIKPRLENPS
                                                                                                                                                                                                                                                                 FMQGGEEMLRXKGGNDNSYNAGDAVNEFDWSR------
                                                                                                                                                                                                                                                                                                  GSPVGYTSSPVETINYVSAHDNETLFDIVSIKTPIGLSIDGECRINHLASSMIALSQGIP
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Pred. No. 2e-37;
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726

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844 832 784 800

724 746 565

430 526 370 486 314 446

394 196

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C:Species: Klebsiella pneumoniae
C:Date: 13-Jan-1995 #sequence_revision 13-Ja
C:Accession: S11823; A32880
R:Kornacker, M.G.; Pugsley, A.P.
Mol. Microbiol. 4, 73-85, 1990
A:Title: Molecular characterization of pula
A:Reference number: S11823; MUID:90205629
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A; Residues: 1-1090 KKOR>
A; Cross-references: EMBL: X52181; NID: 943912;
R; D'Enfert, C.; Pugsley, A.P.
J. Bacteriol. 171, 3673-3679, 1989
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A;Cross-references: GB.M29097; NID:g342046; PIDN:AAA61976.1; PID:g643577 C;Keywords: glycosidase; hydrolase; polysaccharide degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Klebsicila pneumoniac pulS gene A;Reference number: A32880; MUID:89291709 A;Accession: A32880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N;Alternate names: pullulanase
C;Species: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                   F-----TDRYLKLTPTTVSQQVSMRFP----HL----SSYAAFKLPDNANVDELLQG
                                                                                                                                                                                                                                                                                          QKATTFKVWAPTSTQVNVLLYDSATGSVTKIVPMTA-SGHGVWEATVNQNLENWYYMYEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VPGEAVTAVENQA--VIHLVDIAGITSSSAADYSSKNLYLWN---
                                   PVFDLATVNEFSDKVADIQQPFSRLCEVNSAVKSSEFAGYCDSGSTVEEVLNQLKQSDSQ 544
                                                                                                               AKMTTHESHTRDLSAWDQTVPAELRGKYLAL - - - TAGDSNMVQHLKTLSASGVTHVELL
                                                                                                                                                 EDEVIYEMDVRDFSI-DPNSGMKNKGKYLALTEKGTKGPDNVKTGIDSLKQLGITHVQLM 515
                                                                                                                                                                                          TVYHPQSRKVEQYEVTDPYAHSLSTNSEYSQVVDLNDSALKPDGWDNLTMPHAQKTKADL
                                                                                                                                                                                                                              TGQGSTRTAV-----DPYATATAPNGTRGMIVDL--AKTDPAGWNS----DKHTTPKNT
                                                                                                                                                                                                                                                                  DGGVTFRVWAPTAQQVDVVVY-SADKKVIGSHPMTRDSASGAWSWQGGSDLKGAFYRYAM
                                                                                                                                                                                                                                                                                                                                             ET-----VAIAAAEDGILISATQVQTAG------VLDDA-YAEAAEALSYGAQLA
                                                                                                                                                                                                                                                                                                                                                                                 ESGVKTDLVTVTLGEDPDVSHTLS_QTDGYQAKQVIPRNVLNSSQYYYSGDDL--GNTYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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25.3%;
NWGYDPRNYDVPEGQYATNANGNARIKEFKEMVLSLHREHIG
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C:Species: Hordeum vulgare (barrey)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-Oct-1999
C:Accession: T04277
V: Dimarkat V: Lash. R.: Svendsen, I.; Svenson, B
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T04377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable alpha-dextrin endo-1,6-alpha-glucosidase (EC 3.2.1.41) -
N;Alternate names: pullulanase
C:Species: Hordeum vulgare (barley)
                                                                                                                                                                                                                                                                                                         A; Introns: 21/3; 70/1; 87/3; 124/1; C; Keywords: glycosidase; hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-904 <LOK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Description: Isolation and characterization of starch debranching enzyme, A; Reference number: 215320
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                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source: cv. Igri
                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: EMBL: AF022725;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession:
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Best Local :
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                                                                                                                                        92
GVWEATVNONLENWYYMYEVTGOGSTRTAV-----DPYATAIAPNGTRGMIVDL--AKT
                                                         ----DDMFAYTG-PLGAVFSEDSVSLHLWAPTAQGVSVCFFDGPAGPALETVQLKES-N
                                                                                                                                  FPFISS----YRAFKVPSS-VDVASLVKCQLVVASFGADGK-----HVDVTGLQLPGVL- 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LVVAINAAPESRTLNEFAGETLQLSAIQQTAGENSLANGVQIAADGTVTLPAWSVAVL 1073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RDSYDSGDWFNRVDYSLQDNNYNVGMPRISDDGSNYEVITRVKEMVATPGEAELKQMTAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YVTSHDNYTLMDKIALSNPNDSE-ADRIKMDELAQAVVMTSQGVPFMQGGEEMLRXKGGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LASLSDDQVRHLADLTRLGMAGNLADFVMTDKDGAAKKGSEIDYNGAPGGYAADPTEVVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNVLNSSQYYYSGDDLGNTYTQKATTFKVWAPTSTQVNVLLYDSATGSVTKIVPMTASGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IIVVYNPNKTVATINLPSGK-WAINATSGKVGESTLGQ-----AEGSVQVPGISMMIL 945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YQELTELRKSSPLFTLGDGSAVMKRVDFRNTGSDQQAGLLVMTVDDGMKAGASLDSRLDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YSGLIHLRLDHPAFRMTTANEINSHLQFLNSPENTVAYELTDHVN------KDKWGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YVSKHDNQTLWDMISYKASQEADLATRVRMQAVSLATVMLGQGIAFDQQGSELLRSKSFT 895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NQS--DRFETASQINLKGTGIGTFSDRLRDSVRGGGPFDSGDALRQNQGIGSGAGVLPNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTSALPDDQLLTKGAQKGMGVAVFNDNLRNAL-DGNVFDS-----SAQGFATGA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RPMVQKFIIDSLKYWVNEYHIDGFRFDLMALLGKDTMSKAASELHAINPGIALYGEPWTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VN--MDVVYNHTFATQISD----FDKIVPEYYYR-----TMIQVIIPTDQVLEMKLXAE
                                                                                                                                                                                                                  233;
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                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                 15.5%;
                                                                                                                                                                                                                  138;
                                                                                                                                                                                                              Score 786.5; DB 2;
Pred. No. 4.1e-37;
8; Mismatches 277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                      NID: 92502057; PIDN: AAD04189.1;
                                                                                                                                                                                                                                                                                                                               169/3;
                                                                                                                                                                                                                                                                                                                           235/2;
                                                                                                                                                                                                                                                                                                                               285/2;
                                                                                                                                                                                                                Indels 187;
                                                                                                                                                                                                                                                   Length
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B 5 B

Query Match 15.2%; Score 771; DB 2; Length 964; Best Local Similarity 26.0%; Pred. No. 3.5e-36; Matches 260; Conservative 133; Mismatches 320; Indels 286; Gaps 39; y 196 LAGTFQHIFGGSDWAPDN	IBSULT 10 151324 ILlulanase - spinach Species: Spinacia oleracea (spinach) Species: Spinacia oleracea (spinach) Species: O7-May-1995 #sequence_revision 01-Sep-1995. #text_change 09-Sep-1997 Saccession: SS1324 Species: O7-May-1995 #sequence of a cDNA of the Spinacia oleracea L. starch debranching enzyme. Reference number: SS1324 Species: SS1324 Species: Preliminary Status: Prelimina	194 GVMSVTGPREMENRYLYEVDVYHPTKAOVLKCLAGDEYARSLSANGARTMLYDINNETL 253 41 DPAGMINDKHITPKNIEDEVYEMDROD'SI DENSGMKKKYLALTEKCTKGPDNV 497 11
RESULT 11 A25879 alpha-dextrin endo-1,6-alpha-glucosidase (EC 3.2.1.41) precursor - Klebsiella pneumon N.Alternate names: pullulan 6-glucanohydrolase; pullulanase (;Species: Klebsiella pneumoniae C;Date: 30-Jun-1988 *sequence_revision 30-Jun-1988 *text_change 06-Dec-1996 C;Accession: A26879; S02472 R;Katsuragi, N.; Takizawa, N.; Murooka, Y. J. Bacteriol. 169, 2301-2306, 1987	Qy 789 AQAVWMTSOGVPFWQGGEEMLRXKGGNDNSYNAGDAVNEFDWS	OW CSASSVOGSELOGSLANGERAYNESKYTEANHADIGNGSYTLEASKATAALKETDAGIEGY 128 OY 253 SDNINLTVPAGG-AHIT-FSYLESTHAVDTINNEHADLOVESGVKTDLVTVTLGEDD 308 DD 129 DWKIKLDKDOGGLPANVTEKFFHIRGYSAFKAP-ATLDOVESGVKTDLVTVTLGEDD 308 OY 309 DVSHTLSIOTDGYQAKQVIPRINLNSSGYTYGGDDLGHTYTQKATTEKVHAPTSAGG 183 OY 309 DVSHTLSIOTDGYQAKQVIPRINLNSSGYTYGGDDLGHTYTQKATTEKVHAPTSTOWNU 368 DD 184 ACRINTGIJOPG

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670

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A:Title: Entire nucleotide sequence of the pull
A:Reference number: A26879; MUID:87194626
A:Notc: K. aerogencs
A:Accession: A26879
A:Molecule type: DNA
A:Residues: 1-1096 <KAT>
A:Experimental source: strain W70
R:Charalambous, B.M.; Keen, J.N.; McPherson, M.
EMBO J. 7, 2903-2909, 1988
A:Reference number: S02472; MUID:89030658
A:Recession: S02472
A:Status: not compared with conceptual translat
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A:Residues: 1-74 <CHA>
A:Roto: part of this sequence was confirmed by protein sequencing C:Genetics:
A:Gene: pulA
A:Gene: pulA
C:Reywords: glycosidase: hydrolase: polysaccharide degradation F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-1096/Product: alpha-dextrin endo-1,6-alpha-glucosidase #status
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          HIGVN--MDVVYNHTFATQISD----FDKIVPEYYYR-----
                                                                          DSKDNPQVQALNTLVAQTDSYNWGYDPFHYTVPEGSYATDPEGTARIKEFRTNIQAI-KQ
                                                                                                                                                                                                                                                                                                                                                                                                                                 TYTQKATTFKVWAPTSTQVNVLLYDSATGSVTKIVPMTA-SGHGVWEATVNQNLENWYYM 405
                                                                                                                                                        ELLPYFOLATVNEFSDKVADIQQPFSRLCEVNSAVKSSEFAGYCDSGSTVEEVLTQLKQN
                                                                                                                                                                                                  QLMPVFASNSVDE-TDPTQD-------
                                                                                                                                                                                                                                         ADLAKMTIHESHIRDLSAWDQTVPAELRGKYLALTAQ----ESNMVQHLKQLSASGVTHI
                                                                                                                                                                                                                                                                               KNIEDEVIYEMDVRDFSI-DPNSGMKNKGKYLALTEKGTKGPDNVKTGIDSLKQLGITHV
                                                                                                                                                                                                                                                                                                                         YAMTVYHPQSRKVEQYEVTDPYAHSLSTNSEYSQVVDLNDSALKPEGWDGLTMPHAQKTK
                                                                                                                                                                                                                                                                                                                                                               YEVTGQGSTRTAV-----DPYATAIAPNGTRGMIVDL--AKTDPAGWNS----DKHITP
                                                                                                                                                                                                                                                                                                                                                                                                     --TDSGVTFRVWAPTAQQVELVIY-SADKKVIASHPMTRDSASGAWSWQGGSDLKGAFYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QVESGYKTDLYTYTLGEDPDYSHT---LSIQTDGYQAKQYIPRNYLNSSQYYYSGDDLGN 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ****----KVAADS--NGEFSDKYVKLTPTTVNQQVSMRF---PHLASYPAFKLPD-DV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DLPEGNYQYKVALNDSWNNSYPSDNINLTVPAGGAHVTFSYIPSTH-AVYDTINNPNADL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RTVSVIAGNSAVYDSRADAFRAAFGVALADAHWV--DKTTLLWPGGENKPIVRLYYSHSS 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DVTAVLAG-----TFQHIFG----GSDWAPDNHSTLL-----KKVTNNLYQFSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AEDAAKPAVSNAYLDASNOVLVKLSQPLTLGEGXSGFTVHDDTANKDIPVTSVKDASLGQ 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AVASADIPGNPSQVGIIVRTQDW----TKDVSADRYIDLSKGNEVWLVEGNSQIFYNEKD 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VPGEAVQASARQA--VIHLVDIAGITSSTPADYATKNLYLWN-----NETCDALS 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----LLQGDDGGIAESDGILSLSHPGADRRRA-GRYLCRRAEALSYGAQL--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence of the pullulanase MUID:87194626
                                                                                               ---NWGYDPRNYDVPEGQYATNANGNARIKEFKEMVLSLHRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -DWNDVSTTPTGSDKY-----GPYWVI------ 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  147;
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Pred. No. 1.
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A;Gene: pulA
C;Keywords: glycosidase; hydrolase; lipoprotein; polysacc
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-1038/Product: pullulanase #status experimental <MAT>
                                                                                                                                                                                          A;Cross-references: GB:M12503; NID:g149223; R;Kornacker, M.G.; Boyd, A.; Pugsley, A.P.; Mol. Microbiol. 3, 497-503, 1989 A;Title: Klebsiella pneumoniae strain K21: 6 A;Reference number: S04864; MUID:89343636
                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-1038 <JANN
A;Cross-references: EMBL:L19312
A;Experimental source: ATCC 15050
R;Chapon, C.; Raibaud, O.
J. Bacteriol. 164, 639-645, 1985
A;Title: Structure of two divergent promoters
A;Reference number: A91807; MUID:86033821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C:Species: Klebsiella pneumoniae
A:Variety: ATCC 15050; strain K21
C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_C
C:Accession: S38801: A25025; S04864
R:Janse, B.J.H.; Steyn, A.J.C.; Pretorius, I.S.
Curr. Genet. 24, 400-407, 1993
A:Title: Regional sequence homologies in starch-degrading
A:Reference number: S38801; MUID:94130317
A:Accession: S38801
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S38801
                                                                                                              A; Molecule type: protein
A; Residues: 'X', 21-31, 'X', 33, 'X'
A; Experimental source: strain K21
                                                                                      C; Genetics:
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A; Residues: 1-65 < CHA>
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                                                                                         AD-RIKMDELAQAVVMTSQGVPFMQGGEEMLRXKGGNDNSYNAGDAVNEFDWSR--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QIFYNEK------DAEDA------AKPAVSNAYLDASNOVLVKLSOPLTLGEG
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VGMPRISDDGSNYDVISRVKEMVA: PGEAELKQMTAFYRELTGLRKSSPLFTLGDGSAVM
                                                             LNTRVRMQAVSLATVMLGQGIAFDQQGSELLRSKSFTRDSYDSGDWFNRVDYAMQDNNFN
                                                                                                                          LADFILIDKDGAVKKGSEIDYNGAPGGYAADPTEVVNYVSKHDNOTLWDMITYKAAQQAD
                                                                                                                                                          TGATGLTD----AIKNGVE-----GSINDFTSSPGETINYVTSHDNYTLWDKIALSNPNDSE 779
                                                                                                                                                                                                                                                                                                                                                    -FDKIVPEYYYR-----TMIQVIIPTDQVLEMKLXAERPMVQKFIIDSLKYWVNEYHID
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SHLCEVNSAVKSSEFAGYCTSGSTVEEVLNQLKQSDSQDNPQVQALNTLVAQTDSYNWGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.3%; Score 721.5; DB 2
25.5%; Pred. No. 2.6e-33;
                             ---KAQYPDVFNYYSGLIHLRLDHPAFRMTTANEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
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A; Medicus rye: DNA
A; Molecule type: DNA
A; Residues: 1-666 <ARN>
A; Residues: 1-666 <ARN>
A; Cross-references: GB:AE001278; GB:AE001273; NID:g3328423; PIDN:AAC67632.1;
A; Cross-imental source: serotype D, Strain UW-3/Cx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable glycogen hydrolase (debranching) - Chlamydia trachomatis (serotype D, C;Species: Chlamydia trachomatis C;Date: 13-Sep-1998 *sequence_revision 13-Sep-1998 *text_change 08-Oct-1999 C;Accession: E71565
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Science 282, 754-759, 1998
A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlam A;Reference number: A71570; MUID:99000809
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C;Superfamily: glyX protein
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DHVNKDKWGNIIVYYNPNKTVATINLPSGKWAINATSGKVGESTLG
                                                                                                                                                                                                                                                                                                                                                       IIDSLKYWVNEYHIDGEREDLMALLGKD-----TMSKAASELHAINPGIALYGEPW- 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --GSTRTA-----VDPYATAI-----APNGTRGMIVDLAKTDPAGWNSDKHITPKNI- 456
                                                                                                                                                                                                                                      VEGSINDFTSSPGETINYVTSHDNYTLWDKIALSNPNDSEADRIKMDELAQ------
                                                                                                                                                                                                                                                                                                          TGGTSALPDDQLLTKGAQKGMGVAVFNDNLRNALDGNVEDSSAQGFATGATGLTDAIKNG
                                                                                                                                                                                                                                                                                                                                                                                                                                   AGIEVILDVVFNHTGFEGTSCPLPWIDLESYYMVNDHGDLMNFSGCGNTVNTNTPTTLKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -EDEVIYEMDVRDFSIDPNSGMKNKGKYLALTEKGTKGPDNVKTGIDSLKQLGITHVQLM 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DLSSOKFATDSYIADPYSKNIYSPQLFGSPKQEKDYAFSYLKHEDFDWEGD---TPLHLP 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FSLFSSQAQQVTLVLLDPL--SEIHEIPLSSTDHRTGAIWHIEIAGISSEWSYAYKLRGT 83
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                                                                                         SRKAQYPDVFNYYSGLIHLRLDHPAFRMTT--ANEINSHLQFLNSP----ENTVAYELT 883
                                                                                                                                                                                                                                                                                 AGGLYQLGHFPSISTRWSEWNG--CYRDHYKAFLNGDAHQVSS--FASRISGSHDIYPNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EHIGYNMDYVYNHT-FATQISDFDKIVPEYYYRTMIQVIIPTDQVLEMKLXAERPMVQKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIFEFDETVHPFKNQDFPHLCNYWGYSSVNFFCPSRRYTYGADPCAPAREFKTLVKALHR
                                                      DRLAERKELFSFLCQVIALRKAYTELFNTSFLSEDTITWLNTKGSPREWGADHYLAFEL-
                                                                                                                              GETTDPTICALRERQMKNFFLALFLSQGIPMIQSGDEYGHTAYGNNNHWCLDTKINYFLW
                                                                                                                                                                   -----AVVMTSQGVPFMQGGEEMLRXKGGNDNSYNAGDAVNEFDW
                                                                                                                                                                                                        -----KPTNSINYICSHDGFTLYDTVAYNDKHNEENGEYNRDGTSANYSYNFGCE
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A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-666 <TET>
A:Gross-references: GB:AE002298; GB:AE002160; NID:g7190343; PIDN:AAF39177.1; PID:g71903!
A:Experimental source: strain Nigg (MoPn)
C:Gene: TC0312
A:Gene: TC0312
C:Superfamily: glyX protein
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GB1717

glycosyl hydrolase family protein TC0312 [imported] - Chlamydia muridarum (strain Nigg glycosyl hydrolase family protein TC0312 [imported] - Chlamydia muridarum (strain Nigg glycosyl hydrolase family protein TC0312 [imported] - Chlamydia muridarum (strain Nigg C.) Species: Chlamydia muridarum, Chlamydia trachomatis MoPn

C; Species: 11-Mar-2000

C; Accession: GB1717

R; Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzber, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzber, Nucleic Acids Res. 28, 1397-1406, DeBoy, R.; Kolonay, J.; McClarty, G.; Salzber, A; Reference number: AB1500; MUID:20150255

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Best Local Similarity
Matches 177; Conserv
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  583 EWTPDHYLAFEL-KHPN---YSLFIAFYSGNERI-EIALPKLRQE-HLAYEKIVDSTTG
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                                               ---PENTVAYELTDHVNKDKWGNIIVVYNPNKTVATINLPSGKWAINATSGKVGESTLG 929
                                                                                             CLDTKINHFLWDRLAERKEFFSFLCQIITLRITHA -- ELFNTNFLSEETITWLNSQGLPR
                                                                                                                           NAGDAVNEFDWSRKAQYPDVFNYYSGLIHLRLDHPAFRMTTANEINSH-LQFLNS-----
                                                                                                                                                                                               SANYSYNFGCEGETTDPNICQLRERQMKNFFLALFLSQGIPMIKSGDEYGHTAYGNNNHW
                                                                                                                                                                                                                                                                                                                           ATGLTDAIKNGVEGSINDFTSSPGETINYVTSHDNYTLWDKIALSNPNDSEADRIKMD--
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                                                                                                                                                                                                                                                                                            ISGSRDIYPAG--NSTN-----SINYICSHDGFTLYDSVAYNHKHNEENGENNRDGT
                                                                                                                                                                                                                                                                                                                                                                                                                                       -- TALYGEPW-TGGTSALPDDQLLTKGAQKGMGVAVFNDNLRNALDGNVFDSSAQGFATG
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                                                                                                                                                                                                                                          ----ELAQ----AVVMTSQGVPFMQGGEEMLRXKGGNDNSY
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$77094

glycogen operon protein (EC 3.2.1.-) glgX-2 - Synechocystis sp. (strain PCC 6803)

N:Alternate names: protein slr1857

C:Species: Synechocystis sp.
A:Variety: PCC 6803

A:Variety: PCC 6803

C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000

C:Accession: $77094

C:Accession: $77094
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C:Superfamily: glyx protein
C:Keywords: glycosidase; hydrolase
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A;Title: Sequence analysis of the genome of the unicellular cyanobacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Reference number: S74322; MUID:97061201
A;Accession: S77094
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                                               VSQGVPMLLMGDEMGKTQDGNNNTYCHDSPFNWLNWHLLEQNQAWFRFVKHCIAFRLAHP
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*Klebsiella pneumoniae puls gene encodes an oute lipoprotein required for pullulanase secretion.*

J. Bacteriol. 171:3673-3679(1989).

-I - CATALYTIC ACTIVITY: STARCH-DD-DEBRANCHING ENZYM (1-6)-ALPHA-GLUCOSIDIC LINKAGES IN PULLULAN FORM MALFOTRIOSE.
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Structure of two divergent promoters encoding pullulanase in Klebsiella pne regulated by the malT product ";

J. Bacteriol. 164:639-645(1985).
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"Molecular characterization of pulA and i secreted enzyme of Klabsiella pneumoniae Mol. Microbiol. 4:73-85(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-62 FROM N.A. MEDLINE-86033621; Pubmed-3
                                                                                                   Pfam; PF00128; alpha-amylase; 1. PROSITE; PS00013; PROKAR_LIPOPROTEIN;
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LASLSDDQVRHLADLTRLGMAGNLADFVMIDKDGAAKKGSEIDYNGAPGGYAADPTEVVN
                                                        GTSALPDDQLLTKGAQKGMGVAVFNDNLRNAL-DGNVFDS-
                                                                                                       RPMVQKFIIDSLKYWVNEYHIDGFRFDLMALLGKDTMSKAASELHAINPGIALYGEPWTG
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01-AUG-1988 (Rel. 08, La
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PULLULANASE PRECURSOR (E
GLUCOSIDASE) (PULLULAN 6
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J. Bacteriol. 169:2301-2306(1987).
-!- CATALYTIC ACTIVITY: STARCH-DEBR
                                                                                                                                                                       the European Bloinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                 LIPID
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SIGNAL
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PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
                                                                                                                                     EMBL; M16187; AAA25124.1; ALT_SEQ.
PIR; A26879; A26879.
                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; |
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CATALYTIC ACTIVITY: STARCH-DEBRANCHING ENZYME,
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                                                                                                                    TINYVTSHDNYTLWDKIALSNPNDSEAD-RIKMDELAQAVVMTSQGVPFMQGGEEMLRXK
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                                          SFTRDSYDSGDWFNRVDYSLQDNNYNVGMPRSSDDGSNYDIIARVKDAVATPGETELKQM
                                                                       GGNDNSYNAGDAVNEFDWS-----
                                                                                                    VVNYVSKHDNQTLWDMISYKAAQEADLDTRVRWQAVSLATVMLGQGIAFDQQGSELLRSK
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RA Krohn B.M., Barry G.F., Kishore G.M.;
RA Krohn B.M., Barry G.F., Kishore G.M.;
RA Krohn B.M., Barry G.F., Kishore G.M.;
RT "An isoamylase with neutral ph optimum from a Flavobacterium species:
RT Cloning, Characterization and expression of the iam gene.";
RT HOL. Gen. Genet. 254:469-478(1997).
CC CLEANE PULLULAN, HAS A PH OPTIMUM OF 6-7.
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CC C. TINIKAGES IN GLYCOGEN, AMYLOPECTIN AND THEIR BETA-LIMITS DESTRING.
CC C. SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY. ISOAMYLASE SUBFAMILY.
CC C. This SWISS-PROT entry is copyright. It is produced through a collaboration
CC Chies SWISS-PROT entry is copyright. It is produced through a collaboration
CC Chesen the Swiss Institute of Bioinformatics and the EMBL outstation-
CC Chesen the Swiss Institute of Bioinformatics and the EMBL outstation its
CC Cuse by non-profit institutions as long as its content is in no way
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                                IAPNGTRGMIVD -- LAKTDPAGWNSDKHI-----
                                                               IKNTYGITGAVYYGYRAWGPNWPYDAAWTKGSATGFVSDVDNAGNRFNPNKLLLDPYARE
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15-DEC-1998 (Rel. 37,
15-DEC-1998 (Rel. 37,
ISOAMYLASE PRECURSOR
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                                                                                                                                                                                                                                                                      STRAIN-JD210;
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STRAIN-SB-15;
                                                                                                  Biochim.
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                                                                                           Then J.H., Chen Z.Y., Chow T.Y., Chen J.C., Ta
Nucleotide sequence and expression of the iss
isoamylase-hyperproducing mutant, Pseudomonas
Blochim. Biophys. Acta 1087:309-315(1990).
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"Transcription of the isoamylase gene amyloderamosa SB-15.";
J. Bacteriol. 171:4320-4325(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (S or send an email to license@isb-sib.ch).
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Pfam; PF00128; alpha-amylase;
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CATALYTIC ACTIVITY: HYDROLYSIS
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SIMILARITY: BELONGS TO FAMILY
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KNOWN AS THE ALPHA-AMYLASE FAMILY ISOAMYLASE
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VRGFTEQDTSIPAQYRGTYYGAGLKAS-
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F -> C (IN REF. 1).

GAS -> AH (IN REF. 1).

L -> V (IN REF. 1).

GAYT -> AVH (IN REF. 1).

SGLDLFAEPMAIGGNSYOLGGFPQGWSEWNGLFRDS ->

TVWICLRNLGFSAATRTSWVDSRTVVRVEWSVPRQ (IN REF. 1).

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WP -> S (IN REF. 1).

AFRKAHPA -> RSARHIP (IN REF. 1).

AFRKAHPA -> RSARHIP (IN REF. 1).

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P26501;
         EMBL; M25247; AAA25855.1;
EMBL; A10909; CAA00929.1;
PIR; A37035; A37035.
HSSP; P10342; 1BF2.
                                                                     This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Hioinformatics institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
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Bacteria; Proteobacteria,
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GEN. MICCODIOI. 135:37-45(1989).

CATALYTIC ACTIVITY: HYDROLYSIS OF 1.6-ALPHA-D-GLUCOSIDIC LINKAGES IN GLYCOGEN, AMYLOPECTIN AND THEIR BETA-LIMITS [
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SIMILARITY: BELONGS TO
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Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

A Davies R., Devlin K., Feltwell T., Gentles S., Hamiln N., Holroyd S.,

Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J.,

A Oliver S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J.E.

Taylor K., Whitchead S., Barrell B.G.;

"Deciphering the biology of Mycobacterium tuberculosis from the

"Complete genome sequence.";

"La Nature 393:537-544(1988).

C. -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO

KNOWN AS THE ALPHA-AMYLASE FAMILY. STRONG, TO E.COLI AND
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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InterPro; IPR000461; -.
Pfam; PF00128; alpha-amylase;
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                                                                                                                    QYATNANGNARIKEFKEMVLSLHREHIGVNMDVVYNHT----FATQISDFDKIVPEYYYR
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RESULT 8
GLGX_HAEIN
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01-NOV-1995 (Rel. 32, Last ann
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MEDLINE=95350630; PubMed=7542800;
Fleischmann R.D., Adams M.D., White O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLGX OR HI1358.
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                                                                                                                                                                                                                        Science 269:496-512(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria;
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                                                                                                                                                                                                                                                         Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.";
                                                                                                                                                                                                                                                                                     Venter J.C.;
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                                                                                 European Bioinformatics Institute. There are no rest by non-profit institutions as long as its content
                                                                                                                                                            SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                       FUNCTION: THIS PROTEIN CATABOLIC OPERON BUT IS
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                                                                                                                SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the ED
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restrictions

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; U32815; ; P10342;

AAC23005.1;

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RESULT 9
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Best Local Sim
Matches 176;
GLGX_ECOLI
P15067; P76693;
01-APR-1990 (Rel
01-NOV-1995 (Rel
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                                                                                                                          MGFCML
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                                                                                                                                                                           KALQV---VLDNRW---LLLINAKAEGQMFHLPNRKWKPQIGTHNV---TLEAQQAELSS
                                                                                                                                                                                                    VAYELTDHVNKDKWGNIIVVYNPNKTVATINLPSGKWAINATSGKVGESTLGQAEGSVQV
                                                                                                                                                                                                                               ANFNEELFELTKQTIALRK-----QIGSLNKDQWWSDENVQWLNIVGEPMTVEDWQNQQT
                                                                                                                                                                                                                                                                                    QKSAVENNRTFAQSGLLMSLLLANGTPMLLAGDEFGNTQYGNNNAYCQD---NEITWLKW
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gen blosynthesis; Hydrolase; Glycosidase.

BY SIMILARITY.

333 33 BY SIMILARITY.
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659 AA;
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 32, Last sequence up 36, Last annotation
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2e-15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *Analysis of the Escherichia coli glycogen gene cluster suggests catabolic enzymes are encoded among the biosynthetic genes.*; Gene 70:363-376(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; J01616; AAA98735.1; ALT_EMBL; U18997; AAA58229.1; -.
EMBL; AE000419; AAC76456.1; -.
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STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
                                                                                                                                                                                                                                                                                                                                                                                                EcoGene; EG10381; glgx.
InterPro; IPR000461;
                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; JT0400; BVECGX. HSSP; P10342; 18F2.
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Bacteria, Proteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00128; alpha-amylase;
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CATABOLIC OPERON BUT IS NOT REQUIRED FOR GLYCOGEN SYNTHESIS.
SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
KNOWN AS THE ALPHA-AMYLASE FAMILY.
CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A STOP
CODON IN POSITION 507.
                                                                                                                LRYGYRVHGPWQPAEGHRFNPAKLLIDPCARQIDGEFKDNPLLHAGHNEP-DYRDNAAIA
                                                                                                                                               WYYMYEVTGQ-----GSTRTAVDPYATAIAPNGTRGMIVDLAKTDPAGWNSDKHIT 452
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nce 277:1453-1474(1997).
                         PDNVKTGIDSLKQLGITHVQLMPV--FASNSVDETDPTQDNWGYDPRNYDVPEGQYATNA
                                                         PKCVVVVDHYDWEDDAPPRTPWGSTIIYEAHVKGLTYLHPEIPVEIRGTYKALGH-----
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60; Conservative
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BY SIMILARITY.
Y -> YY (IN REF. 2).
W; AA9EFC1F67FD0420 C
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P16950;
01-AUG-1990 (Rel. 15, C
01-AUG-1990 (Rel. 15, I
15-JUL-1999 (Rel. 38, I
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AMYLOPULULANASE PRECURSOR (ALPHA-MYLASE/PULJULANASE) [INCLUDES:
ALPHA-AMYLASE (EC 3.2.1.1) (1.4-ALPHA-D-GLUCAN GLUCANOHYDROLASE);
PULLULANASE (EC 3.2.1.41) (1.4-ALPHA-D-GLUCAN GLUCANOHYDROLASE)
(ALPHA-DEXTRIN ENDO-1,6-ALPHA-GLUCOSIDASE)].
                                                                                                                                                                                                 Melasniemi H., Paloheimo M., Hemioe L.;
"Nucleotide sequence of the alpha-amylase-pullulanase Clostridium thermohydrosulfurioum.";
J. Gen. Microbiol. 136:447-454(1990).
                             FIBRONECTIN TYPE III DOMAINS MEDLINE=93028390; PubMed=140 Bork P., Doolittle R.F.;
                                                                                                                                                           SEQUENCE OF 32-39.
STRAIN-E101-69;
                                                                                                                                                                                                                                                                                                                                           Thermoanaerobacter thermohydrosulfuricus (Clostridium thermohydrosulfuricum)
Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                    Biochem.
                                                                                                   pullulanase
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acquisition of an animal protein domain l. Acad. Sci. U.S.A. 89:8990-8994(1992).
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                                                                                  on and some properties of produced by Clostridium 250:813-818(1988).
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or send an email to license@isb-sib.ch).
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Unpublished observations (NOV-1994).

-I- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.
-I- CATALYTIC ACTIVITY: STARCH-DEBRANCHING ENZYME, HYDROLYZES (1-6)-ALPHA-GLUCOSIDIC LINKAGES IN PULLULAN AND STARCH TO FORM MALTOTRIOSE.
                                                                                                                                                        Ramcsh M.V., Podkovyrov S.M., Lowe S.E., Zeikus J.G.; "Cloning and sequencing of the Thermoanaerobacterium B6A-RI apu gene and purification and characterization amylopullulanase from Escherichia coll."; Appl. Environ. Microbiol. 60:94-101(1994).
                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-1994 (Rel. 29, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
AMYLOPULLULANASE PRECURSOR (ALPHA-AMYLASE/PULLULANASE) (INCLUDES:
ALPHA-AMYLASE (EC 3.2.1.1) (1,4-ALPHA-D-GLUCAN GLUCANOHYDROLASE);
PULLULANASE (EC 3.2.1.41) (1,4-ALPHA-D-GLUCAN GLUCANOHYDROLASE)
QALPHA-DEXTRIN ENDO-1,6-ALPHA-GLUCOSIDASE)).
                                                                                                                                                                                                                                                                                                                             Thermoanaerobacter saccharolyticum.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Thermoanaerobacter group; Thermoanaerobacterium.
                                                                                                                                                                                                                                           MEDLINE-94161525; PubMed-8117096;
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                                                                                                     VPMTASG --
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                                               MIVDLAKTDPAGWNSDKHITPKNIEDEVIYEMDVRDFSIDPNSGMKNKGKYLALTEKGTK
                                                                        LPMTRIGESPDGNYEYWEIKLSFDHPTRIWYYFILKDG---TKTAY--YGDNDDQLGGLG
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                                                                                                                                                                                                                                                                                                          SGFTVHDDTANKDIPVTSVKDASLGQDVTAVLAGTFQHIFG-GSDWAPDNHST-LLKKVT
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IPR001777;
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ETHRONECTIN TYPE-III.
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Pred. No. 1e-10;
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                                                             Thermoanaerobacter ethanolicus (Clostridium thermohydrosulfuricum) Bacteria; Firmicutes; Bacillus/Clostridium group; Thermoanaerobacter group; Thermoanaerobacter.
                                                                                                                                                                                                                                                                                                                      01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
AMYLOPULLULANASE PRECURSOR (ALPHA-AMYLASE/PULLULANASE) [INCLUDES:
ALPHA-MYLASE (EC 3.2.1.1) (1.4-ALPHA-D-GLUCAN GLUCANOHYDROLASE),
PULLULANASE (EC 3.2.1.1) (1.4-ALPHA-D-GLUCAN GLUCANOHYDROLASE)
QALPHA-DEXTRIN ENDO-1,6-ALPHA-GLUCOSIDASE)].
                                                                                                                                                                                                                       SEQUENCE
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SUBUNIT: MONOMER.
SIMILARITY: BELONGS TO FAMILY 13 OF
KNOWN AS THE ALPHA-AMYLASE FAMILY.
SIMILARITY: CONTAINS 2 FIBRONECTIN T
                                                       (1-6)-ALPHA-GLUCOSIDIC FORM MALTOTRIOSE.
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VYNHTFATQI---
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6; Mismatches
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"Pullulanase of Thermoannerobacterlum thermosulfurigenes EM1
(Clostridium thermosulfurogenes): molecular analysis of the ger
composite structure of the enzyme, and a common model for its
attachment to the cell surface.";
J. Bacteriol. 176:3295-3302(1994).
-!- CAPALTTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC
LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.
-!- CAPALTTIC ACTIVITY: STARCH-DEBRANCHING ENZYME, HYDROLYZES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-1994 (Rel. 30, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
AMYLOPULIULANASE PRECURSOR (ALPHA-AMYLASE/PULIULANASE) (PULIULANASE TYPE II) [INCLUDES: ALPHA-AMYLASE (EC 3.2.1.1) (1.4-ALPHA-D-GLUCAN GLUCANOHYDROLASE); PULLULANASE (EC 3.2.1.41) (1.4-ALPHA-D-GLUCAN GLUCANOHYDROLASE) (ALPHA-DEXTRIN ENDO-1,6-ALPHA-GLUCOSIDASE)].
       between
                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-DSM 3896 / EM1;
MEDLINE-94252998; PubMed-8195085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thermosulfurogenes).
Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                   KNOWN AS THE ALPHA-AMYLASE FAMILY.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAL SIMILARITY: CONTAINS 3 S-LAYER HOMOLOGY (SLH) DOMAINS.
                                                                                                                                                    SUBCELLULAR LOCATION:
S-LAYER ANCHOR.
                                                                                                            PTM: GLYCOSYLATED.
SIMILARITY: BELONGS TO FAMILY 13
                                                                                                                                                                                      FORM MALTOTRIOSE
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SWISS-PROT entry is copyright. It is produced through a collaboration -
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InterPro; IPR001777;
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FIBRONECTIN TYPE-III.
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01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
CYCLOMALTODEXTRINASE (EC 3.2.1.54) (CDASE) (CYCLOMALTODEXTRIN
                                                                                         the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oguma T., Matsuyama A., Kikuchi M., Nakano E.;
"Cloning and sequence analysis of the cyclomaltodextrinase gene
Bacillus sphaericus and expression in Escherichia coli cells.";
Appl. Microbiol. Biotechnol. 39:197-203(1993).

-i- FUNCTION: HYDROLYZES CYCLODEXTRINS. CAN ALSO ACT ON LINEAR
MALTODEXTRINS, MITH THE EXCEPTION OF MALTOSE. THE PH OPTIMUM
PH 8.0 AND THE OPTIMAL TEMPERATURE IS 45 DECREES C.

-i- CATALTIC ACTIVITY: CYCLOMALTODEXTRIN + H(2)0 - LINEAR
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Bacteria; Firmicutes; Bacillus/Clostridium
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SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY. CDASE MOST CLOSELY RESEMBLES NEOPULLULANASE FROM B.STEAROTHERMOPHILUS AND ALPHA-AMYLASE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: MONOMER.
                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                               PULLULANASE FROM C. THERMOHYDROSULFURICUM
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Hydrolase; Glycosidase.
ACT_SITE 327 327 BY
ACT_SITE 356 356 BY
ACT_SITE 423 423 BY
SEQUENCE 591 AA; 67899 MW;
                                                                                                                                                      01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-JUL-1993 (Rel. 26, Last annotation update)
CYCLOMALTODEXTRINASE (EC 3.2.1.54) (CDASE) (CYCLOMALTODEXTRINASE HYDROLASE, DECYCLING).
          MEDLINE-92355516; PubMed-1644767
Podkovyrov S.M., Zeikus J.G.;
Structure of the gene encoding
                                                                                                                                                                                                                             CDAS_THEET P29964;
                                                                      SEQUENCE FROM
                                                                                                                          Thermoanaerobacter ethanolicus (Clostridium thermohydrosulfuricum). Bacteria; Firmicutes; Bacillus/Clostridium group;
  thermohydrosul furicum
                                                                                                                Thermoanaerobacter
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                                                                                                                                                                                                                                                                                                                                                                                                                                 MEWDKSKQNTELLAFFRSMISLRKAHPALR-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LTLCSGN----VERMKLATLFQ---LTYQGTPCIYYGDEI-----GMDGEY--
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135; Conservative
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                                                                                                                                                                                                                                            STANDARD;
                                          PubMed=1644767;
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BY SIMILARITY.
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CONFLICT
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"Analysis of the catalytic center of cyclomaltodextrinase from Thermoanaerobacter ethanolicus 39E.";

FEBS Lett. 317:259-252(1993).

-1- FUNCTION: HYDROLYZES CYCLODEXTRINS, CAN ALSO ACT ON LINEAR MALTODEXTRINS, WITH THE EXCEPTION OF MALTOSE.

-1- CATALYTIC ACTIVITY: CYCLOMALTODEXTRIN + H(2)0 - LINEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000461; Pfam; PF00128.
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J. Bacteriol. 174:5400-5405(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MALTODEXTRIN.
SUBUNIT: MONOMER.
                               LPDDQLLTKGAQKGMGVAVFNDNLRNALDGNVFDSSAQGFATGA---TGLTDAIKNGVEG
                                                                                                                                    GYDFFAFQ--DVIKNGKKSKYWDWFNIYEWPIKTHGKPSYEAFADTVWRMPKLMTKNPEV
                                                                                                                                                                                                                                                                                                                                                                           VDLAKTDPAG--W-----NSDKHITPKNIEDEVIYEMDVRDFSIDPNSGMKNKGKY 483
                                                                                                                                                                                                                                                                                                                                                                                                             KIKPMVLTHTNELFDYYETTLELNKKFVYFFYLVSDGGEKL-----YYTE------
LRGDQF------DSVMNYPFRNA----VVDFFAKRKISASRFNTMITEQLMRHMD-
                                                                   QKYLLEVAEYWIKEVDIDGWRLDVANEIDHHFWRKFREVVKAAKPEAIIVGEVWHDASPW
                                                                                                   QKFIIDSLKYWVNEYHIDGFRFDLMALLGKDTMSKAASELHAINPGIALYGEPWTGGTSA 685
                                                                                                                                                                        ----FATQISDFDKIVPEYYYRTMIQVI---IPT-----DQVLEM-KLXAERPMV
                                                                                                                                                                                                      HKYD-TTDYYTIDPHFGDT------QKARELVQKCHDNGIKVIFDAVFNHC
                                                                                                                                                                                                                                      DETDPTQDNWGYDPRNYDVPEGQYATNANGNARIKEFKEMVLSLHREHIGVNMDVVYNHT
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                                                                                                                                                                                                                                                                                                         LALTEKGTKGPDNVK-------TGIDSLKQLGITHVQLMPVFASNSV 523
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Copyright (c) 1993 - 2000 Comp
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O81638 zea mays (m

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O95788 hordeum vul

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O84046 chlamydia t

O9rm63 myroides od

O9pkz6 chlamydia m
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		82	9.4	474.5
	10	78	9.5	480.5
		73	9.7	491.5
	_	71	9.8	497.5
		70		505.5
	10	78	10.0	506
		702	10.0	508

ALIGNMENTS

RESULT Q9XDB5

Q9XDB5

PRELIMINARY;

PRT;

849 ₹

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ACCOUNT REPORT OF THE PROPERTY OF THE PROPERTY
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MEDLINE-99240435; PubMed-10224005;

MEDLINE-99240435; PubMed-10224005;

MEDLINE-99240435; PubMed-10224005;

MEDLINE-99240435; PubMed-10224005;

Pertoido C., Duffner F., Jorgensen P.L., Antranikian G.;

Pertoido C., Duffner F., Jor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 28.2
Best Local Similarity 34.9
Matches 339; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1999
01-NOV-1999
01-MAY-2000
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01-MAY-2000 (TrEMBLrel.
PULLULANASE TYPE I.
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STRAIN-DSM 9078;
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Bacteria; Thermotogales; Fervidobacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       LSVITLIVFALSI----SFAE---TELIIHYHRWDGNYDGWNLWIWWVEPISKEGAAYQF 65
                                                                                                                FYNEKDAEDAAKPAVSNAYLDASNQVLVKLSQPLTLGEGXSGFTVHDDTANKDIPVTSVK 184
                                                                                                                                                                                                                                                                                             NQPADSFGAVASADIPGNPSQVGIIVRTQDW-TKDVSADRYIDLSKGN-EVWLVEGNSQI 124
Y-----TTKP-----DTSPRVL----
                                                                                                                                                                                                                           TE-KDDFGVVAKVKFPETLTKVGIIVRLGEWREKDVAMDRFITIKDGKAEVWLLQGIEQI 124
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(TrembLrel. 12, Last sequence update)
(TrembLrel. 13, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28.2%; Score 1428.5; D
34.9%; Pred. No. 2e-78;
Live 146; Mismatches 3
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                                                                                                                                                                                                       01-FEB-1997
01-FEB-1997
01-MAY-2000
SEQUENCÉ FROM N.A.
STRAIN-5482;
                                                                  Bacteroides thetaiotaomicron Bacteria; CFB group; Bactero NCBI_TaxID-818;
                                                                                                                                                                                   PULLULANASE.
                                                                                                                                                                                                                                                                                                                      P71095
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FINAL PROBLEMS OF THE PROBLEMS
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7 (TrEMBLrel.
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Last sequence update)
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                                                                                                         Bacteroides
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Best Local S
Matches 266
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D'Elia J.N., Salyers A.A.;
"Contribution of a neopullulanase, a puglucosidase to growth of Bacteroides ti J. Bacteriol. 178:7173-7179(1996).

EMBL; U67061; AAC44685.1;
INTERPRO; IPRO00461;
INTERPRO; IPRO00461;
PFAM; PF00128; alpha-amylase; 1.
                                      Q59319 PRELIMINARY; PRT; 825 AA.
Q59319;
Q1-NOV-1996 (TrEMBLrel. Q1, Created)
Q1-NOV-1996 (TrEMBLrel. Q1, Last sequence update)
Q1-MAY-2000 (TrEMBLrel. Q1, Last sequence update)
ALPHA-DEXTRIN 6-GLUCANOHYDROLASE (EC 3.2.1.41)
(ALPHA-DEXTRIN ENDO-1,6-ALPHA-GLUCOSIDASE) (PULLULANASE)
(PULLULAN 6-GLUCANOHYDROLASE) (LIMIT DEXTRINASE) (DEBRANCHING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
  Caldocellum
                            (AMYLOPECTIN
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                                                                                                                                                                                                                VIDVRGLGIQNGPEVIIPSQSALILYK
                                                                                                                                                                                                                                                                                    QGGEEMLRXKGGNDNSYNAGDAVNEFDWSRKAQYPDVFNYYSGLIHLRLDHPAFRMTTAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EV----TGQGSTRTAVDP--YATAIAPNGTRGMIVDLAKTDPAGWNSDKHITPKNIEDEV 460
                                                                                                                                                                                                                                           KVGESTLGOAEG-SVQVPGISMMILHO
                                                                                                                                                                                                                                                                       QVRKHLEFLPVEGSNLIAFRLKDHANGDHWEDIIVAFNSRPTPARLTIPVGKYTVVCKGG
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                                                                                                                                                                                                                                                                                                                                                                                                               -- NDFTSSPGETINYVTSHDNYTLWDKIALSNPNDSEADRIKMDELAQAVVMTSQGVPFW
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 saccharolyticum
                               6-GLUCANOHYDROLASE)
 (Caldicellulosiruptor
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starch.";
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                                          ENZYME]
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AC 06
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DT 01
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Best Local 9
Matches 247
 069008;
069008;
01-AUG-1998
01-AUG-1998
01-MAY-2000
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Eur. J. Biochem. 0:0-0(0).
-1- CATALYTIC ACTIVITY: STARCH
ALPHA-GLUCOSIDIC LINKAGES
MALTOTRIOSE.
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Thermoanaerobacter group; Caldicellulosiruptor.
NCBI_TaxID=44001;
[1]
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                                                                                                                                                                                        KTVATINLPSGKWAINATSGKV-GESTLGQAEGSVQVPGISMMILHQE
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                                                                                                                                                                                                                                             FYCDLINLRRKHIAFRMRSSGEIKKYLRFIPAPDGVVAFIIT--YPYDEWKKIIVAYNPF
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%; Pred. No. 8.3e
122; Mismatches
Last sequence up
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3e-61;
les 244;
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Best Local Similarity
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Submitted (APR-1998) to the EMBL/GenBank/DDBJ
EMBLAGG0205; AAC15073.1;
INTERPRO; IPRO00461;
PFAM; PF00128; alpha-amylase; 1
SEQUENCE 718 AA; 80446 MM; 8F7C0D22405EA8#
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Bacteria; Thermus/Deinococcus
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                                                                                                                                                                                                                                                                                                                                                                                          669
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:::| | | | | ::| |:|||||:| |:| |
PAF------DDRFFYDG-PLGAEYLKEQTVERVWAPTATAVSVKLVHPHLDEI- 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AYLDEMDQIVV--LAPKSLGFDGMAPFTL-VAPSGEEIPLSVQHVEDVGETVKYVCRFAS
                                                                                                                                          ATGLTDATKNGVEGS---INDFTSSPGETINYVTSHDNYTLWDKIALSNPNDSEADRIKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TFOHIFGGSDWAPDNHSTLLKKVTNNLYQFSGDLPEGNYQYKVALNDSWNNSYPSDNINL
  ATINLPSGK-WAINATSGKVGESTLGQAEGSVQVPGISMMIL
                                                  LIALRRAHGAFRLATEAEVLRHFTFLEPLPPSVIAYRLHDAAVYGPWEDIIVVHHNEEKE
                                                                              LIHLRLDHPAFRMTTANEINSHLQFLNS-PENTVAYELTDHVNKDKWGNIIVVYNPNKTV
                                                                                                                                                                                          DELAQAVVMTSQGVPFMQGGEEMLRXKGGNDNSYNAGDAVNEFDWSRKAQYPDVFNYYSG
                                                                                                                                                                                                                                        NPGGREQVKLAIAGSLRALGGLECHPRQSINYVECHDNHTFWDKMEAANHDEPEWLRRKR
                                                                                                                                                                                                                                                                                                                                          DPSILVYGEGWDLPTPLPPEQKATMANAKQLPRFAYFNDRFRDAVKGSTFHLPDRGFALG
                                                                                                                                                                                                                                                                                                                                                                    NPGIALYGEPWTGGTSALPDDQLLTKGAQKGMGVAVFNDNLRNALDGNVFDSSAQGFATG
                                                                                                                                                                                                                                                                                                                                                                                                                                   ANGTGVGNDIASERRMARRWIVDSVVFWAKEYGIDGFRFDLMGVHDIETMKAVRDALDAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KT-----KLAPPSLPLPPLCSPTDAIIYELSIRDFTSHPDSGAVHKGKYLGLAETN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KIVPMTASGHGVWEATVNQNLENWYYMYEVTGQGSTRTAVDPYATAIAPNGTRGMIVDLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TVPAGGAHVTFSYIPSTHAVYDTINNPNADLQVESGVKTDLVTVTLGEDPDVSHTLSIQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative 124;
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L.9e-60;
hes 293;
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Best Local :
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01-OCT-2000
01-OCT-2000
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
EMBL; APO01518; BAB06983.1;
SEQUENCE 717 AA; 81865 MW; 2A979DFA25638920 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus halodurans,
Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
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STRAIN-C-125 / JCM 9153;
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697
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                            931 AEG-SVQVPGISMMILHQ
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                                                                                                                                                                                                                                             459
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FNCHTVSVQSRSSMVLYR
                                                                                                                                                                                                                                                                         KGAQKGMG.VAVFNDNI.RNALDGNVFDSSAQGFATGATGLTDAIKNGVEGSINDFTSSPG
                                                                                                                                                                                                                                                                                                                         KYWVNEYHIDGFRFDLMALLGKDTMSKAASELHAINPGIALYGEPWTGGTSALPDDQLLT
                                                                                                                                                                                                                                                                                                                                                                                                 VNMDVVYNHTFATQISDFDKIVPEYYYRTMIQVIIPTDQVLEMKLXAERPMVQKFIIDSL
                                                                            SPENTVAYELTDHVNK-DKWGNIIVVYNPNKTVATINLP-SGKWAINATSGKVGESTLGQ
                                                                                                                    HGEGNSYNSPDWINOLDWSRRAIYAADVEYVKGLIALRKAHRAFCFSTFSEVNTHMCPLK
                                                                                                                                                                                                                                                                                                         TYWASEYRVDGFRFDLMGIIDQMTMKEVKRALAPINRQILLLGEGWDLET-PLENDQKTT
                                                                                                                                                                                                                                                                                                                                                                    VILDVVFNHVYVMKESPFEKLVPGYYFRYDGEGNLADGTGVGNDIASERLMVRKFIVDCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PVFASNSVDETDPTQD-NWGYDPRNYDVPEGQYATNA-NGNARIKEFKEMVLSLHREHIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DGDLHQYCYLYRAKVNGKWKTTVDPYAKSVTVNGEKGV1FDLKRTDPASWPTVHP1PP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NQNLENWYYMYEVTGQGSTRTAVDPYATAIAPNGTRGMIVDLAKTDPAGWNSDKHITPKN 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QYVYNG-ELGALYSHERTVFAVWTPVATEVSLLLYENWHTLEAIEYQMKRSPNGVWSVSL
                                                       TPSEVIGFHY-HHIAKWGPWDEMVVLHNGGGDKVDIRLPASGEWEVIVDGKKAGLVPLYT
                                                                                                                                                GGNDNSYNAGDAVNEFDWSRKAQYPDVFNYYSGLIHLRLDHPAFRMTTANEINSHLQFLN
                                                                                                                                                                                  QAIQYVEAHDNHTLWDKLQFVFPDEEEEEVLRACHRLATAIVLTSQGIPFLHGGQEFFRTK
                                                                                                                                                                                                             ETINYVTSHDNYTLWDKIALSNPNDSEADRIKMDELAQAVVMTSQGVPFMQGGEEMLRXK
                                                                                                                                                                                                                                                                                                                                                                                                                               PVADYGSVDEANREKEYNWGYDVVIIYFAPEGSYASDPYDGVTRVKELKQLIAQCQRMDLR
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                                                                                                                                                                                                                                             LAQARAVPFLHFFHDTFRDAVKGSTFDLNKGGFCAGNIELKETLIASMLGHEAQF-DRPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            - EHTIIYELHIRDATVYPGSGHHKKGTYLSLAEQNTCGPWGESTGLSYIRELGVTHLELL
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232; Conserv
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15,
                            947
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1084.5;
Pred. No. 1.1e
18; Mismatches
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1.1e-57;
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RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.A.

RA Chol S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

RA Chol S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

RA Chol S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

RA Chol S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

RA Chol S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

RA Brits C., Errington J., Fabret C., Ferrari E., Foulger D.,

RA Fritz C., Fujita M., Fujita Y., Founs S., Galizzi A., Galleron N.,

RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,

RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,

RA Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,

RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,

RA Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,

RA Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,

RA Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,

RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,

RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,

RA Parro V., Pohl T.M., Portetelle B., Rapport G., Rey M., Reynolds S.,

RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,

RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,

RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,

RA Vinters P., Wipat A., Yanamoto H., Waller H., Weitzenegger T.,

"The Complete genome sequence of the gram-positive bacterium Baciilus

RT subtilis.";

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Best Local
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01-JAN-1998 (
01-JAN-1998 (
01-MAY-2000 (
AMYX PROTEIN.
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Azevedo V., I
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Submitted (JUN-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                               EMBL; AF008220; AAC00283.1;
EMBL; Z99119; CAB14971.1; -.
INTERPRO; IPR000461; -.
                                                                                                                                                                                                                    Kunst F., Ogasawara N., Yoshikawa H., Danchin Submitted (NOV-1997) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus/Staphylococcus
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                                                                                                                                                                                                                                                         STRAIN-168;
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                Nature
 234 EGNYQYKVALNDSWNNSYPSDNINLTVPAGGAHVTFSYIPSTHAVYDTINNPNADLQVES 293
                                                                                                                              PF00128; alpha-amylase;
NCE 718 AA; 81104 MW;
                                                                                                                                                                                                                                                                                                              390:249-256(1997).
                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ogasawara N., Moszer
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                                     Conservative
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                                                     20.5%;
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13,
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                                  Score 1039.5;
Pred. No. 5.8e
25; Mismatches
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01-OCT-2000 (TrEMBLrel. 15, Last annotati
DUTATIVE BI-FUNCTIONAL PROTEIN (SECRETED)
SC10B7.21C.
                                                                                                                                                                                                                                                           Q9KZ11
                                                                                                                                                    Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
STRAIN-A3(2);
Cerdeno A.M., Parkhill J., 1
Submitted (MAY-2000) to the
                                                               STRAIN=A3(2);
Seeger K.J., Harris
Submitted (MAY-2000)
                                                                                                                             Actinomycetales; Streptomycineae; NCBI_TaxID=1902;
                                                                                                    SEQUENCE FROM N.A.
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 Barrell B.G., Rajandream
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EIN (SECRETED ALPHA-AMYLASE/DEXTRINASE)
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SEQUENCE FROM
STRAIN-A3(2);
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EMBL; AL355752; CAB90874.1; ".
EMBL; AL355752; CAB90874.1; ".

EMBL; AL355752; CAB90874.1; ".
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                             VLYGEGWNFGEVA-
                                                          ALYGEPWTGGTSALPDDQLLTKGAQK---GMGVAVFNDNLRNAL-DGNVFDS--SAQGFA
                                                                                       ENAMMGKLVVDSVVTWAKEYKVDGFRFDLMGHHPKANILAVRKALDELTLRKDGVDGKKI
                                                                                                                                                                                                               PDCDLAALPAGSEKQQECVTKAAAKDAFNWGYDPYHYTVPEGSYATDPDGTERTVEFRKM
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                                                                                                                  ERPMVQKFIIDSLKYWVNEYHIDGFRFDLMALLGKD---TMSKAASELHAINPG----I
                                                                                                                                                   VKALNEDGLRVVMDVVYNHTAASGQAKTSVLDRIVPGYYQRLLADGSVANSTCCS-NTAT
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                             DDARFVQATQKNMAGTGIATFSDRARDAVRGGGPFDEDPGVQGFA
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Pred. No. 2.5e
49; Mismatches
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No. 2.5
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Best Local Similarity
Matches 296; Conserv
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01-CCT-2000 (TrEMBLrel. 15, Created)
01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
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ALKALINE AMYLOPULLULANASE.
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STRAIN-C-125 / JCM 9153;
TAKAMI H., Nakasone K., Takaki Y.;
Takami H., Nakasone K., Takaki Y.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP001519; BAB07416.1; ...
SEQUENCE 1072 AA; 120674 MW; 5264235CF24619D9 CRC64;
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Bacteria; Firmicutes; Bacillus/Clostridium
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NCBI_TaxID-86665;
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GPPPHAGEKGKPDHASK 1070
                                                                                                                                                            EGFEKREDAIIYEVHVRDFTSDP--GIEEELTAQFGTFASFVDK------LDYIE
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                                                                              IVAVSDPSGFDLTPNEITIDPLTAVIIRVGGDFQENPHDGHPGKGG-GKAKGRPDHAGQP 1053
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PRESILT 9

20983

D p70983

C P70983;

C P70983;

C P70983;

T 01-FEB-1997 (TrEMBLrel. 02, Created)

T 01-FEB-1997 (TrEMBLrel. 15, Last sequence update)

T 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)

E ALKALINE AMYLOPULLULANASE.

E Bacillus sp.

Bacillus sp.

Bacillus p.

Bacillus p.

Bacillus p.

Bacillus p.

Bacillus/Staphylococcus group; Bacillus.

X NCBL_TaxID-1409;

N [1]

P SEQUENCE FROM N.A.

C STRAIN-KSM-1378;
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EMBL; D78258; BAA11332.1; EMBL; D78258; BAA11332.1; EMBL; D78258; TATEONOME.
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INTERPRO; IPRO00834; -.
INTERPRO; IPRO00834; -.
INTERPRO; IPRO01899; -.
PFAM; PF00718; alpha-amylase; 2.
PFAM; PF00716; Gram_pos_anchor; 1.
PFAM; PF00746; Gram_pos_anchor; 2N. 2; UNKNOWN_1.
SEQUENCE 1938 AA; 214917 MW; A29D3F715EB6A
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Kawai S., Watabe T.,
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                                                                                                                                                                                     GEDLKAQFGTFASFVEK------LDYIQELGVTHIQLLPVMSYYFSNEFESGERM
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              HIDGFRFDLMALLGKDTMSKAASELHAINPGIALYGEPWT--GGTSALPDDQLLTKGAQK
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KVDGFRFDMMGDHDAESIQIAFDEAKKLNPNIVMIGEGWVTFAGDEGEPVQAADQQWMQY
                                                                                        NHTFATQISDFDKIVPEYYYRTM1QVIIPTDQVLEMKLXAERPMVQKFIIDSLKYWVNEY
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                                                            NHT--AQVHIFEDLVPNYYH-FMDADGTPRTSFGGGRLGTTHEMSRRVLVDSIKHWVDEY
                                                                                                                                         -TDPTQDNWGYDPRNYDVPEGQYATN-ANGNARIKEFKEMVLSLHREHIGVNMDVVY
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Watabe T., Ito S.;
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25.8%;
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Pred. No. 7.4e-41;
3; Mismatches 369;
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Q9RXB0;
01-MAY-2000
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White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Nakarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.L Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genome Sequence of the Radioresistant Bacterium radiodurans R1.";
Science 286:1571-1577(1999).
EMBL; AE001900; AAF09983.1;
TIGR; DR0405;
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                                                                                                                                    SNQVLVKLSQPL----TLGEGXSGFTVHDDTANKDIPVTSVKDASLGQDVTAVLAGTFQ
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GVSGGDTLA-----LEEVEGGL---
                                                   HIFGGSDWAPDNHSTLLKKVTNNLYQFSGDLPEGNYQYKVALNDSWNNSYPSDNINLTVP 261
                                                                                                      KQQQAIMLSRDLIVVKPALAQPGAWLTLH:
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26.9%; Pred. No. 3.1e
tive 126; Mismatches
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STARCH DEBRANCHING ENZYME.
Oryza sativa (Rice).
Eukaryota; Viridiplantae: Embryophyta; Trachec
Magnollophyta; Liliopsida; Poales; Poaceae; Or
"STRAIN-CV. NORIN-8; Francisco P.B., Zhang
                              SEQUENCE FROM N.A. STRAIN-CV. NORIN-B
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Submitted (ARR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB012915; BAA28632.1; ...
MENDEL; 28470; Orysa;2480;28470.
INTERPRO; IPRO00461; -.
PFAM; PF00128; alpha-amylase; 1.
SEQUENCE 988 AA; 109858 MW; 9D537693EF154A4E CRC64;
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KDAQNEKCKMAQLDKNESYVVTIENVCPHEVSIEIHDLASLGLELHPIQVNSSDALVRQS
                                TDHVNK-----DK-WGNIIVVYN--PNKT----VATINLPSGKWAINATSGKVGES
                                                                                                                                                                                                                                                                                                                                     LYGEGWDFGEVAQNKRGINASQI----NMSGTGIGSFNDRIRDSVNGGNPFGNPLQQGFS
                                                                                                                                                                                                                                                                                                                                                                    LYGEPWTGGTSA-----LPDDQLLTKGAQKGMGVAVFNDNLRNALD-GNVFDSS-AQGFA 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----DPTQD------NWGYDPRNYDVPEGQYATNANGNARIKEFKEMVL 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AWNVNDQDTSLFLYASRDATMHVSDGAIHGYDSKIELEPEHASLPDNVAEKFPFIRS---
                                                                                                                                                                    FMQGGEEMLRXKGGNDNSYNAGDAVNEFDWS-------------
                                                                                                                                                                                                     GSPVGYTSSPVETINYVSAHDNETLFDIVSIKTPIGLSIDEKCRINHLASSMIALSQGIP 784
                                                                                                                                                                                                                                                                     TGLFLEPNGYYQGNEADTRRELAT-YADHIQIGLAGNLKDYVLRTHTGEAKKGSDIYTFD
                                                                                                                                                                                                                                                                                                      TG------ATGLTDAIKNGVEGSIND------
                                                                                                                                                                                                                                                                                                                                                                                                       HEMVDRLTVDDLLNWAINYKVDGEREDLMGHIMKSTMIRAKSAIRSLTRDVHGVYGSKIY
                                                                                                                                                                                                                                                                                                                                                                                                                                      RPMVQKEIIDSLKYWVNEYHIDGFRFDLMALLGKDTMSKAAS-----ELHAI-NPGIA 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLHREHIGVNMDVVYNHTFAT----QISDFDKIVPEYYYRTMIQVIIPTDQVLEMKLXAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AQLAKLPPGSDEQQAAIVSIQQEDPYNWGYDPVLWGVPKGSYASNPDGPSRIIEYRQMVQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -TEKGTKGPDNV-----KTGIDSLKQL---GITHVQLMPVFASNSVDET------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELSDEEPNLESFSDISIYELHIRDFSAHDSTVDCNS----RGGFVHLHFRLFRLNLLNDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --SDKHITPKNIEDEVIYEMDVRDFS----IDPNSGMKNKGKYLAL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VPRYPENQYYLYEVKVYHPSTSQVEKCLADDPYARGLSANGTRTWLVDINSETLKPASWD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DMFAYTG-PLGAVFSDKDVDLYLWAPTAQDVRVCFYDGPAGPLLQTVQLKEL-NGVWSVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SQYYYSGDDLGNTYTQKATTFKVWAPTSTQVNVLLYDSATGSVTKIVPMTASGHGVWEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -YRTFRVPSS-VDVASLVKCQLAVASYDAHGRHQDVT-----GLQLPGVL-----D
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                                                                   PSFRPLKNHILSAFDNFVDILKIRYSSPLFRLSTASDIEQRVRFHNTGPSMVPGVIVMSI
                                                                                                  ---- RKAQYPDVFNYYSGLIHLRLDHPAFRMTTANEINSHLQFLNSPEN----TVAYEL
                                                                                                                                     FFHAGDEILRSKSLDRDSYNSGDWFNKLDFTYETNNWGVGLPPRDKNEENWHLIKPRLEN
                                                                                                                                                                                                                                      ----FTSSPGETINYVTSHDNYTLWDKIALSNPNDSEAD-RIKMDELAQAVVMTSQGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15.9%; Score 805; DB 10; 27.6%; Pred. No. 1.5e-40;
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Best Local Similarity
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081638;
01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
PULLULANASE-TYPE STARCH DEBRANCHING ENZYME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Beatty M.K., Rahman A., Myers A.M., James M.G.;

*Genetic and biochemical characterization of ZPU1, a pullulanase-type starch debranching enzyme from maize.*;

Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; AF080567; AAD11599.1; -.

MENDEL; 32273; Zeama; 2480; 32273.

SEQUENCE 962 AA; 106239 MW; 5F5AAB7C6EBD5D10 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zea mays (Maize).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
MCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-ENDOSPERM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PDVSHTLSIQTDGYQAKQVIPRNVLNSSQYYYSGDDLGNTYTQKATTEKVWAPTSTQVNV
                                  ERPMVQKFIIDSLKYWVNEYHIDGFRFDLMALLGKDTMSKAASELHAI------NPGI
                                                                                                                                                                                                                                                                                                                                                          QDVT-----GLQLPGVL-----DDMFAYTG-PLGTIFSEEAVSMYLWAPTAQDVSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARGLSANSTRTWLYDINNETLKPLAWDGLAAEKPRLDSFSDISIYELHIRDFSAHDSTYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATAIAPNGTRGMIVDL -- AKTDPAGWNSDKHITPK -- NIEDEVIYEMDVRDFSI - DPNSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLIA-----WNISDQKTSLELYASRNATMCMSSQDMKGYDSKVELQPE-NDGLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APRPPMATAEEGASSDVGV-----AVAESAQGFLL------DARAYWVTK
                                                                                                                   QALNRLGLRVVMDVVYNHLYSSGPFAITSVLDKIVPGYYLRRDSNGQTENSAAVN-NTAS
                                                                                                                                                                               LSLHREHIGVNMDVVYNHTFATQ----ISDFDKIVPEYYYRTMIQVIIPTDQVLEMKLXA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLYDSATGSVTKIVPMTASGHGVWEATVNONLENWYYMYEV-----TGQGSTRTAVDPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SDNINLTVPAGGAHVT--FSYIPSTHAVYDTINNPNADLQVESGVKTDLVTVTL---GED
EHFMVDRLIVDDLLNWAVNYKVDGFRFDLMGHIMKKTMIRAKSALQSLTIDEHGVDGSKI
                                                                                                                                                                                                                                          ELSKLPPGSDLQQAAIVAIQEEDPY -- NWGYNPVVWGVPKGSYASNPDGPSRIIEYRLWV
                                                                                                                                                                                                                                                                         Conservative 143; Mismatches 325; Indels 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----VTQKEPE1SS----YRAFRIPSS-VDVATLVKCQLAVASEDAHGNR 185
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Db 96 AWNVNDQDTSLFLYASRDATMHYSDGAIHGYDSKIELEPEHASLPDNVAEKFPFIRS Oy 278 VYDTINNPNADLQVESGVKTDLVTVTLGEDPDVSHTLSIQTDGYQAKQVIPRNV	Query Match 15.7%; Score 793; Best Local Similarity 27.6%; Pred. No. Matches 251; Conservative 134; Mismatc	FT SIGNAL 1 74 POTEN FT CHAIN 75 986 STARC SQ SEQUENCE 986 AA; 109592 MW; FB	INTE PFAM Sign			RC STRAIN-CV. FUJIHIKARI; TISSUE-ENDOSPERN; RX MEDLINE-96275956; PubMed-8680309; RX Nakamura Y., Umemoto T., Ogata N., Kubok	OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta OC Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza. OX NCBI_TaxID-4530; RN [1] RD SEOITENIE FROM N A	DT 01-MAY-2000 (TrEMBLEEL: 03, Last of the Communication of the Communic	AC P93416; DT 01-MAY-1997 (TrEMBLrel 03, Created of 01-MAY-1997 (TrEMBLrel 03 rest of 01-MAY-1997 (TrEMBLR)	RESULT 13 P93416 ID P93416 PRELIMINARY; PRT;	Db 941 DTATGRETVP 950	Qy 929 GQAEGSVQVP 938	Db 881 ARNDRHDMAQIDETFSCVVTVPNVCPYEVS	821	OY 838 ·····DV···FNYYSGLIHLRLDHPAFRI	761	OV 803 OGGEEMLRXKGGNDNGYNAGDAVNEEDWG-	747	Db 641 GLELEPNGFYQGNETETRLTLATYADHIQIGLAGNLKDYVVISHTGEARKGSE	Oy 728 GDAIKI	Db 583 YLYGEGWNFGEVAENQRGINGSQLNMSG
HGYDSKIELEPEHASLPDNVAEKFPFIRS 152GEDPDVSHTLSIQTDGYQAKQVIPRNVLNS 334	a 793; DB 10; Length 986; . No. 8e-40; ismatches 277; Indels 248; Gaps	POTENTIAL. STARCH DEBRANCHING ENZYME. MW; FBABB9E1634CAD27 CRC64;			yme or pullulanase) from developing A and chromosomal localization of the		nyta; Tracheophyta; Spermatophyta; ; Poaceae; Oryza.	annotation update) DR.	od)	; 986 AA.			YATINLPSGKWAINATSGKYGESTL 928 	TTASDIVQRVHFHNTGPSLVPGVIVMSIED 8	FNYYSGLIHLRLDHPAFRMTTANEINSHLOFLNSPENTVAYELTD 884	ETNNWGVGLPPREKNEGSWPLMKPRLENPS	STEMPLSIDERCRINHLSTSMIALSQGIPFF 760	FTSSPGETINYVTSHDNYTLWDKIALSNPNDSEAD-RIKMDELAQAVVMTSQGVPFM 802	: : :: QIGLAGNLKDYVVISHTGEARKGSEIRTFDGS 700	•	

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[1]
SEQUENCE FROM N.A.
*MEDLINE=99169277; Pubmed=10069825;
"MEDLINE=99169277; Pubmed=10069825;
                                                                                                                                                                                                                                       Q9S758 PRELIMINARY; PRT; 962 AA. Q9S758; 01-MAY-2000 (TrEMBLrcl. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence up 01-MAY-2000 (TrEMBLrel. 13, Last annotation LIMIT DEXTRINASE.
                                                                                                                           Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; I
Magnoliophyta; Liliopsida;
MCBI_TaxID-4513;
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Best Local Similarity 27.8%;
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EMBL: AF122050; AAD34348.1; -.
EMBL: AF122049; AAD34347.1; -.
Hydrolase; Glycosidase.

Hydrolase; Glycosidase.
SEQUENCE 962 AA; 105752 MW; 5158386FAED162EE C
                               897
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                                                                                                                                                                                                                  YTLWDKIALSNPNDSEAD-RIKMDELAQAVVMTSQGVPFMQGGEEMLRXKGGNDNSYNAG
                                                                                                                                                                                                                                                                                                                                         VYN--PNK-----TVATINLPSGKWAINATSGKVGESTLGQAEGSVQVPGISMMI 944
                                                                                                                                                                                          ETLEDVISVKTPMILSVDERCRINHLASSMMALSQGIPFFHAGDEILRSKSIDRDSYNSG
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VFNVCPHEVSMDIPALASMGFELHPVQVNSSDTLVRKSAYESATCRFTVPGRTVSV
                                                            IRYSSPLFRLSTANDIKQRVRFHNTGPSLVPGVIVMGIEDARGESPEMAQLDTNFSYVVT
                                                                                LRLDHPAFRMTTANEINSHLOFLNSPENTVAYELTDHVNKDK------WGNIV 896
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01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation updat
LIMIT DEXTRINASE.
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INTERPRO; IPR000461; -. PFAM; PF00128; alpha-amylase; 1. SEQUENCE 904 AA; 99123 MW; C7116CC2DE99ED03 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; E
Magnoliophyta; Liliopsida;
MCBI_TaxID-4513;
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VDGFRFDLMGHIMKRTMVTKSALQSLTTDAHGVDGSKIYLYGEGW--DFAEVARNQRGIN 544
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WFNKLDFTYETNNWGVGLPPSEKNEDNWPLMKPRLENPSFKPAKGHILAALDSFVDILKI
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Search completed: April 22, 2001, 09:10:53 Job time: 354 sec

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879.620 Million cell updates/sec
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4 7 618 20 Y37184	4.7 764 21 Y50819	4.7 164 18 W34879	4.7 818 20 Y17523	.5 4.9 793 20 Y00869	.5 4.9 164 17 R98372	5.5 766 20 Y00870 S	.5 5.6 666 20 ¥34991 (.5 5.7 726 21 Y78515	.5 5.7 726 20 W95636	5.7 745 10 P90615	5.9 750 10 P94419	5.9 776 21 Y78516	6.0 208 20 W81971	6.2 746 19 W53886	6.2 746 17 R92693	52.5 6.3 777 19 W53885	6.3 777 17 R92692	6.3 774 19 W35390	6.4 620 21 B05950	8.0 618 19 W55098	9.2 716 16 R71616	9.4 931 20 Y27357	10.0 243 20 Y04387	633 11.2 1250 21 Y91279 Gr	11.5 893 17 W09257	11.5 798 20 W73552	11.6 772 18 W34567	72.5 11.9 ,772 19 W49871	12.0 658 13 R23787	92.5 12.3 1938 20 W73553	2.3 1938 17 W09255	16 12.7 849 20 Y24380	77 13.8 830 20 Y31747
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ALIGNMENTS

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CCCXSXTTEXTRACTOR
                                                                                                                                                                                                                                                                  RESULT
                                     Gene encoding pullulanase - derived from gene from Klebsiella genus.
                                                                                                                                                                                                                   01-NOV-1990
                                                              WPI; 1988-333488/47.
N-PSDB; N81341.
                                                                                                     31-MAR-1987;
                                                                                                                     31-MAR-1987;
                                                                                                                                                   JP63245676-A.
                                                                                                                                                                   Klebsiella aerogenes.
                                                                                                                                                                                  Pullulanase; starch; alcohol prodn.
                                                                                                                                                                                                  Pullulanase protein
                                                                                                                                                                                                                                   P82507;
                                                                                                                                                                                                                                                  P82507 standard;
                                                                                     (ELED ) DENKI KAGAKU KOGYO KK; (SUNR) SUNTORY LTD
                                                                                                                                    12-OCT-1988
                                                                                                                                                                                                                   (first entry)
                                                                                                     87JP-0078355
                                                                                                                    87JP-0078355
                                                                                                                                                                                                                                                 protein; 1096 AA.
                                             recombinant plasmid pMP1 contg.
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Disclosure; ; p; Japanese.

The pullulanase protein cleaves alpha-1,6-glucoside bonds of starch and is effective in decomposition of branched starch. It is used in the

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GSELLRSKSFTRDSYDSGDWFNRVDYSLQDNNYNVGMPRISDDGSNYEVITRVKEMVATP 945
                           dsalkpegwdgltmphaqktkadlakmtiheshirdlsawdqtvpaelrgkylaltaqes
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glucose. Amir
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                                                                                                                                             Spinach debranching enzyme (DE) (R98371) is useful for modifying the branching degree of amylopectin synthesised in plants. Its amino acid sequence was deduced from a CDNA clone (T31478) derived from spinach leaves. The DE can be obtd. by recombinant expression in procaryotic or eucaryotic host cells. The DE may also be expressed in transgenic plants, e.g. potato. The consequent increase in DE activity results in the blosynthesis of modified starches by the plant. These may have food or industrial applns.
                                                                                                                          Sequence
                                                                                                                                                                                                                                                Claim 1; Page 68-70;
                                                                                                                                                                                                                                                                   DNA encoding a de-branching enzyme - for degree of amylopectin starch synthesised
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                      plkkdssc----fccsmavevgsassvsqselggs
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             Pullulanase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a fragment of a novel Zea mays pullulanase protein. This protein and the encoding nucleic acid fragments may be used to create transgenic plants in which corn pullulanase is present in cells at levels differing from the norm, or in cell types or developmental stages where it is not normally found, in order to alter starch structure in those cells. They may also be used to isolate cDNAs and genes encoding homologous pullulanase from the same or other plant species, to amplify those genes and to produce antibodies for screening of cDNA expression
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                                                            LNQLKQ-SDSQDNPQVQALNTLVAQTDSYNWGYDPFHYTVPEGSYATDPEGTTRIKEFRT
                                                                                                                         aglthvhllpsfqfggvdd
                                                                                                                                                         SGVTHVELLPVFDLATVNEFSDKVADIQQPFSRLCEVNSAVKSSEFAGYCDSGSTVEEV-
                                                                                                                                                                                                                  TMPHAQKTKAD-LAKMTIHESHIRDLSAWDQTVPAELRGKYLALTAGDSNWVQHLKTLSA 476
                                                                                                                                                                                                                                                 rnwenryylyevtvyhqttgniekclaadpyarglsanstrtwlvdinnetlkplawdgl
                                                                                                                                                                                                                                                                                                            --plgtisseeavsmylwaptaqdvsvsfydgp----agplletvqlnelngvwsvtgp
                                                                                                                                                                                                                                                                                                                                          ALSYGAQLADGGVTFRVWAPTAQQVDVVVYSADKKVIGSHPMTR----DSASGAWSWQGG
                                                                                                                                                                                      -aekprldsfsdisiyelhirdfsahdstvdcpfrggfcaftfqdsvgiehlkklsd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25.2%; Score 1419.5; DB 20; 35.7%; Pred. No. 3.5e-99; tive 172; Mismatches 340; 1
                                                                                                                            ----ikg----nwkcvdeie
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host cell
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Gaps

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SAPEHRMFAKLIADSLAVWTTDYKIDGFRFDLMGYHPKAQILSAWERIKALNPD---

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This partial sequence represents a novel debranching enzyme isolated Zea mays (maize). This enzyme has been used in the production of
                                   Claim 1;
                                                       DNA encoding maize de-branching starch in transgenic plants
                                                                                        WPI; 1997-458572/43.
N-PSDB; T93875.
                                                                                                                                                                                           07-MAR-1996;

 mays debranching

                                                                                                                                                                                                                                                                                                                                                                                                                          W34878 standard; Protein; 558
                                                                                                                         Emmermann
                                                                                                                                               (PLAN-) PLANTTEC BIOTECHNOLOGIE
                                                                                                                                                                     07-MAR-1996;
                                                                                                                                                                                                                 11-SEP-1997
                                                                                                                                                                                                                                     DE19608918-AJ
                                                                                                                                                                                                                                                                      Protein
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                                                                                                                                                                                                                                                                                                                                      debranching
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --IXFFGEGWDSN---QSDRFEIASQINLKGTGIGTFSDRLRDSVRGGGPFDSGDALRQN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lenpsfkpakhdilaaldkfidilkiryssplfrlttasdivgrvhfhntgpslvpgviv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VKEMVATPGEAELKQMTAFYQELTELRKSSPLFTLGDGSAVMKRVDFRNTGSDQQAGLLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             glpffhagdeilrsksldrdsydsgdwfnkidftyetnnwgvglppreknegswplmkpr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GIAFDQQGSELLRSKSFTRDSYDSGDWFNRVDYSLQDNNYNVGM-PRISDDGSNYEVITR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tfdgspvgyasspletinyasahdnetlfdlislktpmdls1dercrinhlstsmialsq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qgfstglflepngfyqgnetetrltlatyadhiqiglagnlkdyvvishtgearkgseir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QGIGSGAGVLPNELASLSDDQVR----HLADLTRLGMAGNLADFVMIDKDGAAKKGSEI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              skiylygegwnfgevaengrgingsqlkmsgtgigsfndrirdainggspf--gnplq--
                                 Page 19-21; 13pp; German.
                                                                                                                         ×
                                                                                                                                                                                                                                                                                                                           product.
                                                                                                                                                                                                                                                                                                                                    enzyme;
                                                                                                                                                                                                                                                                                                                                                                               (first
                                                                                                                         Kossmann
                                                                                                                                                                     96DE-1008918
                                                                                                                                                                                          96DE-1008918.
                                                                                                                                                                                                                                                                     Location/Qualifiers
1..558
                                                                                                                                                                                                                                                                                                                                     maize;
                                                                                                                                                                                                                                                                                                                                                           enzyme
                                                                                                                                                                                                                                                                                                                                                                               entry)
                                                                                                                         Ç
                                                                                                                                                                                                                                                         "partial sequence of debranching
                                                                                                                                                                                                                                                                                                                                    transgenic plant;
                                                                                                                         Willmitzer L;
                                                                   enzyme
                                                                                                                                               GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1078
                                                                  useful for
                                                                                                                                                                                                                                                                                                                                    starch;
                                                                 production
                                                                                                                                                                                                                                                                                                                                    food industry;
                                                                                                                                                                                                                                                         enzyme'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                             Pullulanase; pulB; debranching enzyme; amylopectin; thermostable; c genetically engineered variant; wheat; potato; wheat; manioc; rice; starch; sugar production; high fructose syrup; high maitose syrup; maitodextrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transgenic plants in which the nucleic acid is stably integrated in the bost cell's genome and expressed. Such an enzyme can be used in the production of starch which is useful in the food industry or in the production of industrial products e.g. paper, adhesives, textiles, textile care products, building materials, soil stabilisers, agrochemicals, pharmaceutical products, cosmetics, coal briquettes, flocculants for ore and coal slurries, foundry sand binders, rubber
                                                                                                               Pullulanase (pulB) amino acid
                                                                                                                                                  05-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       goods, leather substitutes and polymers.
                                                                                                                                                                                                                 Y78513 standard; protein; 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                          419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         542 SDSQDNPQVQALNTLVAQTDSYNWGYDPFHYTVPEGSYATDPEGTTRIKEFRTMIQAIKQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              602 DLGMNVIMDVVYNHTNAAGPTDRTSVLDKIVPWYYQRLNETTGSVESATCCSDSAPEHRM 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 -lglrvvmdvvynhlyssgpfaitsvldkivpgyylr-rdsngqtensaavnntasehfm 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 sdlq-----qaaivaiqeedpynwgynpvvwgvpkgsyasnpdgpsriieyrlmvqalnr 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GYAADPTEVVNYVSKHDNQTLWDMISYKASQEADLATRVRMQAVSLATVMLGQGIAFDQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GVLPNELASLSDDQVR----HADLTRLGMAGNLADFVMIDKDGAAKKGSEI-DYNGAPG
                                                                                                                                                                                                                                                                                                                                    ADGTVTLPAWSVAVLELPQ 1078
                                                                                                                                                                                                                                                                                                                                                                    ndrhdmaqidetfscvvtvfnvcpyevsieipdlaslrlqlhpvqvnssdalarqsaydt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSELLRSKSFTRDSYDSGDWFNRVDYSLQDNNYNVGM-PRISDDGSNYEVITRVKEMVAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gyasspletinyasahdnetlfdlislktpmdlsidercrinhlstsmialsqgipffha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            egwnfgevaenqrgingsqlnmsgtgigsfndrirdainggspf--gnplq--qgfstgl
                                                                                                                                                                                                                                                                                                                                                                                                                                     PGEAELKQMTAFYQELTELRKSSPLFTLGDGSAVMKRVDFRNTGSDQQAGLLVMTVDDGM 1004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gdeilrsksldrdsydsgdwfnkidftyetnnwgvglppreknegswplmkprlenpsfk 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EGWDSN---QSDRFEIASQINLKGTGIGTFSDRLRDSVRGGGPFDSGDALRQNQGIGSGA 770
                                                                                                                                                                                                                                                                                                                                                                                                       KAG---ASLDSRLDGLVVAINAAP--ESRTLNEFAGETLQLSAIQQTAGENSLANGVQIA 1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       558 AA;
                                                                                                                                                (first
                                                                                                                                                entry)
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Pred. No. 2.2e-67;
0; Mismatches 198;
                                                                                                                                                                                                                   $
                                                                                                               sequence
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                                                                             corn;
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Bacillus acidopullulyticus

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Best Local S
Matches 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           parent enzyme. The enzyme variants are useful for converting starch to one or more sugars. This is useful when starches such as corn, potato, wheat, manioc and rice starch are used as starting materials in commercial large scale production of sugars, such as high fructose syrup, high maltose syrup, maltodextrins, amylose, G4-G6 oligosaccharides and other carbohydrates such as fat replacers. The thermostable debranching enzymes of the invention make it possible to perform liquefaction and debranching simultaneously before the saccharification step. By debranching using the thermostable debranching enzyme variants during liquefaction together with the action of an alpha-amylase, the formation of panose precursors is reduced, thereby reducing the panose content in the final product and increasing the overall saccharification yield.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents a pullulanase amino acid sequence. Pullulanases are debranching enzymes which can attack amylopectin. This sequence represents a parent enzyme from which genetically engineered variant debranching enzymes can be created. The genetically engineered enzyme has an improved thermostability at a pH in the range of 4-6 compared to the parent enzyme. The modified enzyme may alternatively or also have an increased activity towards amylopectin and or glycogen compared to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 29; Fig 3; li6pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Variant bacterial pullulanases and isoamylases having, e.g. increased thermostability, used for converting starch from potatoes into high
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bisgard-Frantzen H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fructose syrup
                                   352
                                                                       249
                                                                                                           292
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296
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                                                                                                                                                                                                                                                                                                                                                                                                  78
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nes 267; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000-160767/14.
wklkvpgnlknwyylyqvtvngktqtav-----dpyvraisvnatrgmivdledt--np
                                WSWQGGSDLKGAFYRYAMTVYHPQSRKVEQYEVTDPYAHSLSTNSEYSQVVDLNDSALKP 411
                                                                                                       LDDAYAEAAEALSYGAQLADGGVTFRVWAPTAQQVDVVVYSADKKVIGSHPMTRDSASGA 351
                                                                                                                                                                           LPDNANVDELLQGETVAIAAAEDGILISAT-QVQTAGV----
                                                                                                                                                                                                                                                                                         ndwsqkntsddlhi---dltkgheiwivqgdpniyynlsda-qaaatpkvsnayldnekt
                                                                                                                                                                                                                                                                                                                                                                                                 ADYSSKNLYLWNNETCDALSAPVADWNDVSTTPSGSDKYGPYWVIPLNKESGCINVIVR- 136
                                                                                                                                       nansassseqtdlvqltlasapd---vshtiqvgaagyeavnliprnvlnlpryyysgnd
                                                                                                                                                                                                                                                   LLWPGGQDKPIVRLYYSHSSKVAADGEGKFTDRYLKLTPTTVSQQVSMRFPHLSSYAAFK
                                                                                                                                                                                                                                                                                                                         -DGTDKLIDSDLRVAFGDFT-DRTVSVIAGNSAVYDSRADAFRAAFGVALAEAHWVDKNT
                                                                       Lgnvysnkata-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      170;
                                                                                                                                                                                                                                                                                                                                                           -pv-ngngaayefsgkddfgvkadvqvpgddtqvglivrt
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 840.5; DB 21;
Pred. No. 3.8e-55;
0; Mismatches 337;
                                                                   frvwaptasdvqlllynsetgpvtkqlemqksdngt
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                         01-APR-1996;
                                                 01-APR-1996;
                                                                                                   JP09271385-A
                                                                                                                                                                Bacillus
                                                                                                                                                                                        Trimmed enzyme protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QQGSELLRSKSFTRDSYDSGDWFNRVDYSLQDNNYNVGMPRISDDGSNYEVITRVKEMVA 943
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PDIYFFGEGWDSNQS--DRFEIASQINLKGTGIGTFSDRLRDSVRGGGPFDSGDALRQNQ
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                         96JP-0134492
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding a trimmed enzyme - enzyme with wide substrate speci
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                                                                                                                                                                                                 LRGKYLAL----TAGDSNMVQHLKTLSASGVTHVELLPVFDLATVNEFSDKVADIQQPFS
                                                                                                                                                                                                                             apngtrgmvvdl--aktnptgwks----dkhmtpkniedevlyemhvrdfsi-dsnsgmt
                                                                                                                                                                                                                                                                                                                 KVIGSHPMT----RDSASGAWSWQGGSDLKGAFYRYAMTVYHPQSRKVEQYEVTDPYAHSL
                                                                                                                                                                                                                                                                                                                                           qtdgfktgrv1prnvldfsqyyysged1--gntytkkattfkvwaptstkvnvllyn---
                                                                                                                                                                                                                                                                                                                                                                      QTAG-----VLD-DAYAEANEALSYGAQLADGGVTFRVWAPTAQQVDVVVYSADK
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                            SYLDKIYPWYYORLNETTGSVESATCCSDSAPEHRMFAKLIADSLAVWTTDYKIDGFRFD
                                                                                                                                                                        nkgkylaltekgtkgpenvktgvdslkqlgithvqlqpvfafnsvde------
                                                                                                                                                                                                                                                         STNSEYSQVVDLNDSALKPDGWDNLTMPHAQKTKADLAKMTIHESHIRDLSAWDQTVPAE
                                                                                                                                                                                                                                                                                      kaagaltktvpmkasghgvwsvtvpqnlenwyylyevtgqgstrtav-----dpyatai
                                                                                                                                                                                                                                                                                                                                                                                                                                  TPTTVSQQVSMRFPHLSSYAAFKLPDNANVDELLQG----ETVAIAAAEDGILISATQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----GTDKLIDSDLRVAFGDFTDRTVSVIAGNSAVYDSRADAFRAAFGVALAEAHWVD
                                                        ydprnynvpegqyatdangttrikefkemvlslhrnhigvn--mdvvynhtfatqisd--
                                                                                                                                           RLCEVNSAVKSSEFAGYCDSGSTVEEVLNQLKQSDSQDNPQVQALNTLVAQTD--SYNWG
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This sequence represents a pullulanase amino acid sequence. Pullulanases are debranching enzymes which can attack amy lopectin. This sequence represents a parent enzyme from which genetically engineered variant debranching enzymes can be created. The genetically engineered enzyme has an improved thermostability at a pH in the range of 4-6 compared to the parent enzyme. The modified enzyme may alternatively or also have an increased activity towards amylopectin and or glycogen compared to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pullulanase; debranching enzyme; amylopectin; thermostable; cogenetically engineered variant; wheat; potato; wheat; manioc; starch; sugar production; high fructose syrup; high maitose symaltodextrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1044
                                                                                                                                                             Variant bacterial pullulanases and isoamylases having, e.g. incohermostability, used for converting starch from potatoes into
                                                                                                                                                                                                                                          Bisgard-Frantzen
                                                                                                                                                                                                              WPI; 2000-160767/14.
                                                                                                                                                                                                                                                                                                     02-JUL-1998;
                                                                                                                                                                                                                                                                                                                                 02-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                               13-JAN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                       Bacillus deramificans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pullulanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-MAY-2000
                                                                                                                                                    fructose syrup
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                                                                                                                      29; Fig 3; 116pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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Query Match
Best Local Similarity
Matches 278; Conserv
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                                                                                                                                                                                                                                                           VPAELRGKYLAL----TAGDSNMVQHLKTLSASGVTHVELLPVFDLATVNEFSDKVADIQ
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DRLRDSVRGGGPFDSGDALRQNQGIGSGAGVLPNELASLSDDQVRHLADLTRLGMAGNLA
                                                                                                   FDLMGYHPKAQILSAWERIKALNPDIYFFGEGWDSNQS--DRFEIASQINLKGTGIGTFS
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                                                                                                                                                       ----fdkivpeyyyrtddagnytngsgtgneiaaerpmvqkfiidslkywvneyhidgfr
                                                                                                                                                                                                            RTSVLDKIVPWYYQRLNETTGSVESATCCSDSAPEHRMFAKLIADSLAVWTTDYKIDGFR
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   Claim
                     New pullulanase from Bacillus deramificans -
saccharification etc., with good stability ov
ranges, also related DNA vectors, transformed
                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                     /note-
Misc-difference 620
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15-JUL-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus deramificans pullulanase precursor.
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 Fig 5;
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                                                                                          DeWeer
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93BE-0000744.
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812
61pp;
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                                                                                                                                                                                                                                                                                                                             Location/Qualifiers 163
                                                                                          70
                                                                                                                                                                                                                                     /note-
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                      camificans - for starch stability over wide temp. transformed cells etc.
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      LASLSDDQVRHLADLTRLGMAGNLADFVMIDKDGAAKKGSEIDYNGAPGGYAADPTEVVN
                                 gtsalpddqlltkgaqkgmgvavfndnlrnal-dgnvfds
                                                                                  rpmvqkfi1dslkywvneyhidgfrfdlmallgkdtmskaaselhainpgialygepwtg
                                                                                                    ----KLIADSLAVWTTDYKIDGFRFDLMGYHPKAQILSAWERIKALNPDIYFFGEGWDS
                                                                                                                                     vn--mdvvynhtfatqisd----fdkivpeyyyr----tmmqviiptdqvlemklxae
                                                                                                                                                                                                         DNPQVQALNTLVAQTDSYNWGYDPFHYTVPEGSYATDPEGTTRIKEFRTMIQAI-KQDLG
                                                                                                                                                         ------nwgydprnydvpegqyatnangnarikefkemvlslhrehig
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Pred. No. 3.2e-51;
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                                                                                                                                                                   28-DEC-1992;
15-JUL-1993;
19-NOV-1993;
This sequence represents the mature pullulanase enzyme isolated from Bacillus deramificans T 89.117D. The pullulanse hydrolyses alpha-1,6-glycosidic bonds of amylopectin and of pullulan. The
                                                                                                                                                                                                                                                                                      /note=
Misc-difference 592
                                                                                                                                                                                                                                                                                                       /note-
Misc-difference 591
                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
Misc-difference 134
                                          Claim
                                                                                                   N-PSDB;
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                                                                               New pullulanase from
                                                                                                                              Amory
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hydrolysis;
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                                         3; F1g
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93BE-0000744.
93BE-0001278.
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783
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                                                           Bacillus deramificans for starch , with good stability over wide temp.

DNA vectors, transformed cells etc.
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                                                                                                                                                                                                                             WYYQRLNETTGSVESATCCSDSAPEHRMFA-----KLIADSLAVWTTDYKIDGFRFDLM
                                                                                                                                                                                                                                                                        PEGSYATDPEGTTRIKEFRTMIQAI-KQDLGMNVIMDVVYNHTNAAGPTDRTSVLDKIVP
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 MQAVSLATVMLGQGIAFDQQGSELLRSKSFTRDSYDSGDWFNRVDYSLQDNNYNVGMPRI
                                            IDKDGAAKKGSEIDYNGAPGGYAADPTEVVNYVSKHDNQTLWDMISYKASQEADLATRVR
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                                                                                                                                                                                                                                                                                                                                            SAVKSSEFAGYCDSGSTVEEVLNQLKQSDSQDNPQVQALNTLVAQTDSYNWGYDPFHYTV
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                                                                                                                                                                                                                                                                                                               -----nwgydprnydv
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                                                                                   ----tgltdalkngvegsindf--
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Misc-difference 591
                                                                                                                                                                                                                                                                                                                /note- 'encoded by Misc-difference 135
                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                              straight chain amylase alpha-1,6-glucosidase.
                                                                                                                                                                                                                                                                              /note- "encoded Misc-difference 592
                                                                                                                                                                                                                                                                                                                                                               Bacillus deramificans
                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Y31746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1046 TAGENSLANGVQIAADGTVTLPAWSVAVL 1074
                                                New modified pullulanase for saccharification of starch
                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                        Pullulanase; enzyme engineering; starch; saccharification; straight chain amylase; alpha-dextrin 6-glucano-hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                   22-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Y31746
                                                                                                                                     04-MAR-1998;
                                                                                                                                                      03-MAR-1999;
                                                                                                                                                                                         W09945124-A2
                                                                                                                                                                                                                                                    Protein
                                                                           N-PSDB; X87941.
                                                                                  WPI; 1999-540851/45
                                                                                                                    (GEMV ) GENENCOR INT INC
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                                                                                                   BS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard; Protein;
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                                                                                                   Shetty JK;
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                                                                                                                                                                                                                                 pullulanase
of Claim 31
                                                                                                                                                                                                                                  used
(see
                                                          aqueous
                                                                                                                                                                                                        in claimed
y31748)"
                                                                                                                                                                                                                                  in claimed Y31747)"
                                                         liquefied
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The present sequence represents Bacillus deramificans strain T89.117D mature pullulanase (EC-3.2.1.41). This enzyme has a pI 4.1-4.5, has a half-life of about 55 hr at 60 deg C and is capable

Claim 31; Fig 1A-E; 49pp; English.

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nucleic acids encoding them, vectors, host cells and methods for creombinant production. The modified pullulanses are useful in the starch industry for the saccharification of aqueous liquefied starch, forming syrups of high glucose and maltose content. Other uses (not claimed) are: as anti-staling additives in bread; in the preparation of oligosaccharides from amylopectin or of the proparation of oligosaccharides from amylopectin or of the proparation of oligosaccharides from amylopectin or of tetraholosides from maltose; to condense mono- or oligosaccharides, or in the pharmaccutical industry (no details). When used for smounts of by-products, especially they provide higher glucose that saccharification, the modified pullulanses reduce the amounts of by-products, especially they provide higher glucose to reversion reaction products. When used with glucosamylase, they make possible a higher level of dissolved solids in the material consecution; friends access in increased productivity and a more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of catalysing the hydrolysis of alpha-1,6-glucosidic bonds in amylopectin and pullulan. The invention relates to the discothat B. deramificans pullulanase recombinantly produced in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus host is modified yet retains the ability to catalyse the hydrolysis of an alpha-1,6-glucosidic bond. The modification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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515 SAVKSSEFAGYCDSGSTVEEVLNQLKQSDSQDNPQVQALNTLVAQTDSYNWGYDPFHYTV
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                                                                                                                 altekgtkgpdnvktgidslkqlgithvqlmpvfasnsvde-tdptqd------
                                                                                                                                                                                   AL---TAGDSNMVQHLKTLSASGVTHVELL,PVFDLATVNEFSDKVADIQQPFSRLCEVN
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Misc-difference 591
04-MAR-1998;
                     03-MAR-1999;
                                                                                                   Misc-difference
                                                                                                                                                                                                                          Bacillus deramificans
                                                                                                                                                                                                                                                                              Bacillus deramificans N-truncated pullulanase.
                                                                                                                                                                                                                                                                                                                                                 Y31748 standard; Protein;
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                                           10-SEP-1999.
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                                                                                                                                                                                         Misc-difference 134
                                                                                                                                                                                                      Key
                                                                                                                                                                                                                                                          Pullulanase;
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                                                                                                                                                                                                                                                        enzyme engineering; starch; saccharification;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity Matches 269; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to condense mono- or oligosaccharides, or in the pharmaceutical industry (no details). When used for starch saccharification, the modified pullulanases reduce the amounts of by-products, especially they provide higher glucose yields in short reaction times, without losses associated with reversion reaction products. When used with glucoamylase, they make possible a higher level of dissolved solids in the material being treated, resulting in increased productivity and a more energy-efficient process.

Note: The present sequence is not shown in the specification but is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  is modified yet retains the ability to catalyse the hydrolysis of an alpha-1.6-glucosidic bond. The modification of the recombinant pullulanase announce to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents an N-terminally truncated pullulanase of Bacillus deramificans strain T89.117D, comprising amino acids 103-928 of the native mature enzyme (see Y31746). The native mature pullulanase (EC-3.2.1.41) has a pI of 4.1-4.5, a half-life of about 55 hr at 60 deg C and is capable of catalysing the hydrolysis of alpha-1,6-glucosidic bonds in amylopectin and pullulan. The invention relates to the discovery that B. deramificans pullulanase recombinantly produced in a Bacillus host seminated the complex of the background of the complex of the complex of the background of the complex of the complex of the background of the complex of the co
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                                                                                                                                               -VLDDA-YAEAAEALSYGAQLADGGVTFRVWAPTA 323
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/note-
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pullulan. The invention relates to the discovery control of the recombinantly produced in a Bacillus host of is modified yet retains the ability to catalyse the hydrolysis of is modified yet retains the ability to catalyse the hydrolysis of the modification of the recombinant of the modification of the signal periodes as well as susceptibility to extracellular proteolytic processing. The invention provides of extracellular proteolytic processing. The invention provides of modified pullulanases, especially N-terminally truncated B. CC modified pullulanases, especially N-terminally truncated B. CC vectors, host cells and methods for recombinant production. The cc modified pullulanases are useful in the starch industry for the saccharification of aqueous liquefled starch, forming syrups of high glucose and maltose content. Other uses (not claimed) are: as
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Matches 269
                                                                                                                                                                                                                                                                                                                                                                                                        high plucose and maltose content. Other uses (not craimed) alto beers; anti-staling additives in broad; in brewing low calorie beers; anti-staling additives in broad; in brewing low calorie beers; production of low calorie foods (where amylose is used as substitute for fat); to clarify fruit juices; in the preparation of oligosaccharides from amylopectin or of tetraholosides from maltose; to condense mono- or oligosaccharides, or in the pharmaceutical industry (no details). When used for starch saccharification, the
                                                                                                                                                                                                                                                                                                                industry (no details). When used for starch saccharification, the modified pullulanases reduce the amounts of by-products, especially they provide higher glucose yields in short reaction times, without losses associated with reversion reaction products. When used with glucoamylase, they make possible a higher level of dissolved solids in the material being treated, resulting in increased productivity and a more energy-efficient process.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents an N-terminally truncated pullulanase of Bacillus deramificans strain T89.117D, comprising amino acids 99-928 of the native mature enzyme (see Y31746). The native mature pullulanase (EC-3.2.1.41) has a pI of 4.1-4.5, a half-life of about 55 hr at 60 deg C and is capable of catalysing the hydrolysis of alpha-1.6-glucosidic bonds in amylopectin and pullulan. The invention relates to the discovery that B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                        Sequence
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                                                179 AFGVALAEAHWVDKN--TLLMPGGQDKPIVRLYYSHSSKVAADGEGKF-----TDRYLK 230
                   76 ifg ---- gsdwapdnhstli----
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                                                                                                                                                       Local Similarity 26.8 les 269; Conservative
                                                                                                    PLNKESGCINVIVRDGT---DKLIDSDLRVAFG-DFTDRTVSVIAGNSAVYDSRADAFRA 178
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Fervidobacterium pennavorans Ven 5 thermostable pullulanase
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N-PSDB; X90036.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amylopullulanase, alpha-amylase and pullulanase can each be expressed in transformed host cells using vectors conty. the appropriate gene fragments. The enzymes are useful as additionally and the control of the contr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding alkaline pullulanase having alkaline alpha-amylase activity - useful for improving the efficacy of dish washing detergents and detergents for clothes, esp. on starch soils
1074 lecikeqleikdvdgndvsftdvtiegektvhvhgefdlekipfsvtyldrtisvksgwk 1133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "nucleotides encoding these residues are present in the coding sequence given in specification"
Misc-difference 1050..1065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New mutant pullulanase - useful in bleach-containing detergents
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nes 281;
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                                                                                                                                                                                                                                                        nkigflfvn------kqsggqtgdmtfdmlk------
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   -rgvwsvkltkdntgldslkgyyyhyeit--
                                   ASGAWSWQ------GGSDLKGAFYRYAMTVYHPQSRKVEQYEVT----DPYAHSLST-NS
                                                                 lidemyaydgk---lgaelhedgtatlkvwspkadnvsvvlydkvdqnevvdtiemvkgd
                                                                                               -LDDAYAEAAEALSYGAQL-ADGGVTFRVWAPTAQQVDVVVYSA--DKKVIGSHPMTRDS
                                                                                                                             leelkegleikdvdgndvsftdvtiegektvhvhgefdlekipfsvtyldrtisvksgwk
                                                                                                                                                            FPHLSSYAAFKLPDNANV---DELLQGETVAIAAAE---DGILISATQV-QTAGV-----
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Similarity 24.2%; Pred. No. 2.6e-43;
81; Conservative 168; Mismatches 387;
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1062	ASLDSRLDGLVVAINAAPESRTLNEFAGETLQLSAIQQTAGENSLANGVQIAADG	1008	B &
1007	AELKOMTAFYQELTELRKSSPLFTLGDGSAVMKRVDFRNTGSDQQAGLLVMTVDDGMKAGglielrrssdafrlgsrelvdsnvtmvdapelkeqdlvvay	948	д
1742		1702	У
947 1701	FTRDSYDSGDWFNRVDYSLQDNNYNVGMPRISDDGSNYEVITRVKEMVATPGE : : : : : : : :	895 1658	g 6
894 1657	TRVRNOAVSLATVMLGQGIAFDQQGSELLRSKS	862 1601	β δ
861	MIDKDGAAKKGSEIDYNGAPGGYAAD-PTEVVNYVSKHDNQTLWDMISYKASQEADLA	805	g
1600		1546	S
804 1545	RDSVRGGGPFDSGDALRQNQGIGSGAGVLPNELASLSDDQVRHLADLTRLGMAGNLADFV : ::	745 1528	B &
744	YHPKAQILSAWERIKALNPDIYFFGEGWDSNQSDRFETASQINLKGT-GIGTFSDRL.744 :	689	A
1527		1468	S
688	DKIVPWYYQRLNETIGSVESATCCSDSAPEHRWFAKLIADSLAVWTTDYKIDGFRFDLMG: : : edlvpnyyhfm-dadgtprtsfgggrlgtthemsrrvlvdsikhwvdeykvdgirfdmmg	629	g
14 6 7		1409	Q
628	HYTVPEGSYATDPEG-TTRIKEFRTMIQAI-KQDLGMNVIMDVVYNHTNAAGPTDRTSVL:	571	ρ
1408		1357	γ
570 1356	CEVNSAVKSSEFAGYCDSGSTVEEVLNQLKQSDSQDNPQVQALNTLVAQTDSYNWGYDPF	511 1340	B 5
510	AELRGKYLALTAGDSNMVQHLKTLSASGVTHVELLPVFDLATVNEFSDKVADIQQPFSRL 510 : : : : :	451	g
1339		1292	₽ 5
450	EYSQVVDLNDSALKPDGWDNL/IMPHAQKTKADLAKMTIHESHIRDLSAWDQTVP 450 ; ; ; ; ; ; ; ; ; ; ; ;	397	₽
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Search completed: April 22, 2001, 08:57:42 Job time: 7283 sec

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Compugen Ltd
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/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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US-08-478-341-11
US-08-961-733-11
US-08-961-083-72
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APPLICANT: RENZ, ANDREAS
TITLE OF INVENTION: DNA MOLECULES CODING FOR
TITLE OF INVENTION: FROM PLANTS
FILE REFERENCE: AGREVO-6
CURRENT APPLICATION NUMBER: US/08/860,339
CURRENT FILING DATE: 1997-11-25
EARLIER APPLICATION NUMBER: DE P4447387.7
EARLIER FILING DATE: 1994-12-22
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 18
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Patent No. 6117665
GENERAL INFORMATION:
APPLICANT: Kossmann, Jens
APPLICANT: Emmermann, Michael
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Searched:

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399
                                                                                                                                         191 LQLPGVIDELY-----
                                                                                                                                                                                                                                                                                                                                                                     183 ALAEAHWVDKNTLLW----PGGQDKPIVRLYYSHSSKVAADGEGKFTDR------YLKL 231
                                                                                                                                                            PLKKDSSC------FCCSMAVEVGSASSVSQSELQGS-----L
SQVVDLNDSALKPDGWDNLT---MPHAQKTKADLAKMTIHESHIRDLSAWDQTVPAELRGK 456
                                                                               PMTR----DSASGAWSWQGGSDLKGAFYRYAMTVYHPQSRKVEQYEVTDPYAHSLSTNSEY 398
                                                                                                                                                                                                                             DKDQGGLPANVTE----KFPHIRGYSAFKAPATLDVDSLLKCQLAVAAFSADGACRNATG
                                                                                                                                                                                                                                                                                                                         NSCRAYWPSKYTFAWNVDIGNGS-----YYLFASKTAA---LKFTDAGIEGYDVKIKL 134
                                           PLQTVQLIESNGVWSAVGPRTWEGCYYVYEITVYHHSTLRIEKSFAIDPYARGISADVKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative 169; Mismatches 324;
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                                                                                                                                       SYDGPLGAVESENTISLYLWAPTAQAVSASIF---KDPSGGE
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                                                                                                                                                                                                                                                                                                                                  Sequence 11, Application US/08474140 Patent No. 5721127
                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,140
                                                                                                                                                                                                 APPLICANT: DEWEER, PHILIPPE
APPLICANT: AMORY, ANTOINE
TITLE OF INVENTION: PULLULANASE, MICROORGANISMS WHICH
TITLE OF INVENTION: PRODUCE IT, PROCESSES FOR THE PREI
TITLE OF INVENTION: PULLULANASE AND THE USES THEREOF
MUNBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      921
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CITY: Washington
STATE: D.C.
                                                                                                              ZIP: 20006
                                                                                                                              COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DIEDRVRFHNNVPSWIPGLIAMSLEDG-HAGAPGLSQIDPKFQYIVVIINVQPTETKFVN 914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLPPKDHNESNWPLI---KKRLANPSYKPDKNHIIAAVENFTNLLQIRYSSPLFRLRSAK 855
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                                                                                                                                                                          E: WILLIAN BRINKS HOFER GILSON & LIONE, P.C 2000 K Street, N.W., Suite 200
                                                                                                                          U.S.A.
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; LENGTH: 928 amino acids
; TYPE: amino acids
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-474-140-11
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Best Local Sim
Matches 282;
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TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
LENGTH: 928 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Wilhlem F. Gadiano, Esq. REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-41
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY_AGENT INFORMATION:
NAME: Wilhlem F. Gadiano,
REGISTRATION NUMBER: 37,1:
                                                                                                                                           515
                                                                                                                                                                                   575
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GYHPKAQILSAWERIKALNPDIYFFGEGWDSNQS--DRFEIASQINLKGTGIGTFSDRLR
                                                                                                                                                            PEGSYATDPEGTTRIKEFRTMIQAI-KQDLGMNVIMDVVYNHTNAAGPTDRTSVLDKIVP
                                                                                                                                                                                                                                                                                                                                                                                 GMIVDL--AKTDPAGWNS----DKHITPKNIEDEVIYEMDVRDFSI-DPNSGMKNKGKYL
                                                                                                                                                                                                                                                                                                                                                                                                          SQVVDLNDSALKPDGWDNLTMPHAQKTKADLAKMTIHESHIRDLSAWDQTVPAELRGKYL 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                KIVPMTA-SGHGVWEATVNQNLENWYYMYEVTGQGSTRTAV-----DPYATAIAPNGTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSHPMTRDSASGAWSWQGGSDLKGAFYRYAMTVYHPQSRKVEQYEVTDPYAHSLSTNSEY 398
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||::|:|||||||:|||||
YQAKQVIPRNVLNSSQYYYSGDDL--GNTYTQKATTFKVWAPTSTQVNVLLYDSATGSVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TPSGSDKY-----GPYWVIPLNKE------SGCINVIVRDGTDKLIDSDLRV 149
                                                        EYYYR-----TMMQVIIPTDQVLEMKLXAERPMVQKFIIDSLKYWVNEYHIDGFRFDLM
                                                                                               WYYORLNETTGSVESATCCSDSAPEHRMFA-----KLIADSLAVWTTDYKIDGFRFDLM
                                                                                                                                       PEGQYATNANGNARIKEFKEMVLSLHREHIGVN--MDVVYNHTFATQISD----FDKIVP
                                                                                                                                                                                                                                                                                                      ALTEKGTKGPDNVKTGIDSLKQLGITHVQLMPVFASNSVDE-TDPTQD------
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                                                                                                                                                                                                                                                              SAVKSSEFAGYCDSGSTVEEVLNQLKQSDSQDNPQVQALNTLVAQTDSYNWGYDPFHYTV
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                                                                                                                                                                                                                        -----NWGYDPRNYDV
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                                                                                               ; TOPOLOGY:
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US-08-477-630-11
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION UMBER: US/08/4
APPLICATION UMBER: US/08/4
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
NAME: Wilhlem F. Gadiano, E
                                                                                                                                                                                                             TELEPHONE: (202) 429-06:
TELEPAX: (202) 293-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
LILIAN BRINKS HOFER GILSON & LIONE,
LICENSES AND LICENSES AND LIONE,
LICENSES AND LICENSE
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-42
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: DEWEER, PHILIPPE APPLICANT: AMORY, ANTOINE
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                                                                                                                                                             TYPE: amino acids
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                                                                                                                   TYPE: protein
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25.4%;
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  Score 788.5; DB 1;
Pred. No. 4.7e-58;
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                                                         NTGSDQQAGLLVMTVDDGMKAGASLDSRLDGLVVAINAAPESRTLNEFAGETLQLSAIQQ 1045
                                                                                                                                                                                                                                                                                               MQAVSLATVMLGQGIAFDQQGSELLRSKSFTRDSYDSGDWFNRVDYSLQDNNYNVGMPRI 925
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NSPENTVAYELTDHVN----
                                                                                                                                                                                         SDDGSNYEVITRVKEMVATPGEAELKOMTAFYQELTELRKSSPLFTLGDGSAVMKRVDFR
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                                                                                                                                                                                                                                                             MDELAQAVVMTSQGVPFMQGGEEMLRXKGGNDNSYNAGDAVNEFDWS--------
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                                                                                                                         RKAQYPDVFNYYSGLIHLRLDHPAFRMTTANEINSHLQFL
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-- KDKWGNIIVVYNPNKTVATINLPSGK-WAINATSG
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; MOLECULE TYPE: protein US-08-472-293-11
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TELEFAX: (202) 293-1850
TELEX: 650 383-5605
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 928 amino
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Best Local Similarity
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Patent No. 5731174
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/472,293
FILING DATE: 07-JUN-1995
GLASSIFICATION: 435
GLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Wilhicm F. Gadiano, Esq.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-44
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1090RMATION:
TELECOMMUNICATION 1090RMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: PULLULANASE, MICROORGANISMS WHICH TITLE OF INVENTION: PRODUCE IT, PROCESSES FOR THE PREPARATION TITLE OF INVENTION: PULLULANASE AND THE USES THEREOF NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:
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CITY: Washington
STATE: D.C.
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ZIP: 20006
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                                                                                                                             -TLLWPGGQDKPIVRLYYSHSSKVAADGEGKF-----TDRYLKLTPTTVSQQVSMRFP- 245
    GGAHVTFSYIPSTHAVYDTINNPNAD--LQVESGVKTDLVTVTLGEDPDVSHTLSIQTDG
                                                                                                                                                                           TLGEGXSGFTVHDDTANKDIPVTSVKDASLGQDVTAVLAGTFQHIFG----GSDWAPDNH 185
                                                                                                                                                                                                                    AFGD----FT--DRTVSVIAGNSAVYDSR------ADAFRAAFGVALAEAHWVDKN- 193
                                                 ---HL-----SSYAAFKLPDNANVDELLQGET-----VAIAAAEDGILISATQVQTAG
                                                                                                                                                                                                                                                                ----ADRYIDLSKGNEVWLVEGNSQIFYNEKDAEDAAKPAVSNAYLDASNQVLVKLSQPL 129
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                                                                                                                                                                                                                                                                                                                                                   AGDYOPWSLWMWPKDGGGAEYDFNQPADSFGAVASADIPGNPSQVGIIVRTQDWTKDVS-73
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                                                                                                                                                                                                                                                                                                                                                                                                                                        14.0%; Score 788.5; DB 1; llarity 25.4%; Pred. No. 4.7e-58; Conservative 151; Mismatches 359;
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                                                                                         -KKYTNNLYQFSGDLP---EGNYQYKVALNDSW--NNPSYPSDNINLTVPA
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                                                                                                                                                                                                                                        Sequence 11, Application US/08474545 Patent No. 5736375
                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                     APPLICANT: DEWEER, PHILIPPE
APPLICANT: AMORY, ANTOINE
TITLE OF INVENTION: PULLULANASE, MICROORGANISMS WHICH
TITLE OF INVENTION: PRODUCE IT, PROCESSES FOR THE PREF
TITLE OF INVENTION: PULLULANASE AND THE USES THEREOF
NUMBER OF SEQUENCES: 15
CORRESPONDENCES: 15
CORRESPONDENCES: LITTAN BEHAVE HOPE'S CHICAN & LITTAN BE
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ADDRESSEE: WILLIAN BRINKS HOFER GILSON & LIONE, STREET: 2000 K Street, N.W., Suite 200 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                       KVGESTLGQ-----AEGSVQVPGISMMIL 917
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (202) 429-0625
TELEFAX: (202) 293-1850
TELEX: 650 383-565
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-43
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 07-JUN-19
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NAME: Wilhlem F. Gadiano,
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MEDIUM TYPE: Floppy disk
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                                                                                AL----TAGDSNMVQHLKTLSASGVTHVELLPVFDLATVNEFSDKVADIQQPFSRLCEVN
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                             SAVKSSEFAGYCDSGSTVEEVLNQLKQSDSQDNPQVQALNTLVAQTDSYNWGYDPFHYTV
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                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,341
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Wilhlem F. Gaddiano, Esq.
REGISTRATION NUMBER: 37,136
REFERENCE/DOCKET NUMBER: 4121-45
TELECOMMUNICATION INFORMATION:
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INFORMATION
                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: PULLULANASE, MICROORGANISMS WHICH TITLE OF INVENTION: PRODUCE IT, PROCESSES FOR THE PREPARATION OF TITLE OF INVENTION: PULLULANASE AND THE USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: DEWEER, PHILIPPE APPLICANT: AMORY, ANTOINE
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STREET: 20
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                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Washington
STATE: D.C.
                                    TELEPHONE: (202) 429-0625
TELEFAX: (202) 293-1850
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                     650 383-5605
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FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                      U.S.A.
                                                                                                                                                                                                                        US/08/478,341
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 928 amino acids
; TYPE: amino acids
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-478-341-11
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Best Local Similarity
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866 MQAVSLATVMLGQGIAFDQQGSELLRSKSFTRDSYDSGDWFNRVDYSLQDNNYNVGMPRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109 TPSGSDKY ----- GPYWVIPLNKE -------SGCINVIVRDGTDKLIDSDLRV 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74 ----ADRYIDLSKGNEVWLVEGNSQIFYNEKDAEDAAKPAVSNAYLDASNQVLVKLSQPL 129
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                                                                                                                                                                                                                                                                                                                                                                        PEGSYATDPEGTTRIKEFRTMIQAI-KQDLGMNVIMDVVYNHTNAAGPTDRTSVLDKIVP
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                                                                                                                NAL-DGNVFDS-----SAQGFATGA------TGLTDAIKNGVEGSINDF--
                                                                        TDKDGAAKKGSETDYNGAPGGYAADPTEVVNYVSKHDNQTLWDMTSYKASQEADLATRYR
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; MOLECULE TYPE: US-08-996-733-11
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Patent No. 6074854
                                                                                                                                                                              APPLICATION UNMER: BE 09300744
FILING DATE: 15-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION UNMBER: BE 09201156
FILING DATE: 28-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Debra J. Glaister, Esq.
REGISTRATION NUMBER: 33,888
REFERENCE/DOCKET NUMBER: GC446C1-US
TELECOMMUNICATION INFORMATION:
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APPLICANT: DEWEER, PHILIPPE
APPLICANT: AMORY, ANTOINE
                                                                                                                          TELEFAX: (6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US
FILING DATE: 23 DEC-1S
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
APPLICATION ON DATA:
FILING DATE: 07-JUN-1S
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: PULLULANASE, MICROORGANISMS WHICH TITLE OF INVENTION: PRODUCE IT, PROCESSES FOR THE PRETITLE OF INVENTION: PULLULANASE AND THE USES THEREOF NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: BE 0
FILING DATE: 19-NOV-1993
                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Rela
CURRENT APPLICATION DATA:
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CITY: Palo Alto,
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 28-DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                     TYPE: amino acids
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                                        TOPOLOGY: linear
                                                                                                                                                             TELEPHONE:
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                                                                                                                                              (650) 845-6504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genencor International, Inc
                                                                                                                          SEQ ID NO:
                                                                                                                                                                 (650) 846-7620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UMBER: US 08/174,893
28-DEC-1993
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                                                                                                        SDDGSNYEVITRYKEMVATPGEAELKOMTAFYQELTELRKSSPLFTLGDGSAVMKRVDFR
                                                                                                                                                                   MDELAQAVVMT SQGVPFMQGGEEMLRXKGGNDNSYNAGDAVNEFDWS
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                                                       ---RKAQYPDVFNYYSGLIHLRLDHPAFRMTTANEINSHLQFL
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Best Local :
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APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
SOFTWARE: ASCII 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER:
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CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 618 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
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                                                                                                 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Human Genome Sciences, STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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                                                                                                                                                                                                                                       GVTHIQLLPVLSYYFVNELKNH---
                              TTHHMTKRLLIDSIKYLVDTYKVDGFRFDMMGDHDAASIEEAYKAARALNPNLIMLGEGW
                                                     PEHRMFAKLIADSLAVWTTDYKIDGFRFDLMGYHPKAQILSAWERIKALNDDIYFFGEGW 716
                                                                                                 NEIHK-RGMGAILDVVYNH-----TAKVDLFEDLEPNYYHFM-DADGTPRTSFGGGRLG 122
                                                                                                                                 QAIKQDLGMNVIMDVVYNHTNAAGPTDRTSVLDKIVPWYYQRLNETTGSVESATCCSDSA 656
                                                                                                                                                                   -----ERLSDYASSNSNYNWGYDPQNYFSLTGMYSSDPKNPEKRIAEFKNLI
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DSNQSDR----FEIASQINLKGTG-IGTFSDRLRDSVRGGGPFDSGDALRQNQGIGSGAGV 772
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SYSTEM: MSDOS version
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                                                                                                                                                                                                                                                                                                       ; Score 449.5; DB 4;
; Pred. No. 1.5e-29;
86; Mismatches 208;
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TELEFAX: (314)537-6047

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 777 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-476-519-2
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Patent No. 5750876
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                  NAME: Bonner, Grace L.
REGISTRATION NUMBER: 32,963
REFERENCE/DOCKET NUMBER: 38-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-7286
TELEFAX: (314)537-6047
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APPLICANT: Kishore, Ganesh M.
APPLICANT: Krohn, Bradley M.
APPLICANT: Klishore, Ganesh M.
APPLICANT: Klishore, G
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS_MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/281902
FILING DATE: 28-JUL-1994
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NAME: Bonner, Grace !
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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CITY: St.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 800
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700 Chesterfield Parkway No. 5750876th
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                                   1019 VAINAAPESRTLNEFAGET------LQLSALQOTAGENSLANGVQIAADGTVTL 1066
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                                                                                                                                                                                                                             PSDGGEDHNLSWNQGGIVAEQRKAARTGLALLMLSAGVPMITGGDEALRTQ-------
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                                                                                                             LRKSSPLFTLGDGSAVMKRVD-FRNTGSDQQAGLLVMTVDDGMKAGA---SLDSRLDGLV 1018
                                                                                                                                                                                       GDWFNRVDYSLQDNNYNVGMPRISDDGSNYEVITRVKEMVATPGEAELKQMTAFYQELTE
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FGDSASAIYVAYNGWSGAVDFKLPWPGTGKQWYRVTDTATWNEGPNAV~~ALPGSETL
                                                                         LRPANFYSASDTNGNVMEQLRWFKPDGAQ------ADSAYFNGADNHALAWRIDGSE 700
                                                                                                                                                     ---EG-----NNNTYNL-----DSAANWLYWSR--SALEADHETYTKRLIAFRKAHPA 649
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                                                                                                                                                                                                                                                                 ---LATRVRMQAVSLATVMLGQG1AFDQQGSELLRSKSFTRDSYDS
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RESULT 10
PCT-US95-09323-2
Sequence 2, Application
GENERAL INFORMATION:

PC/TUS9509323

TITLE OF INVENTION:

Novel Isoamylase Gene, Cor Containing It and Methods

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APPLICANT:

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Best Local Similarity
Matches 203; Conserv
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPOTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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LENGTH: 777 amino acids
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                                                                                                                                                                        FDSG-----DALRQNQGIGSGAGVLPNELASLSDDQVRHLADLTRLGMAGNLADFV
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                                                                   -NDLYGDDGRKPWHSINFVVAHDGFTLNDLYAYNDKQNNQPWPYG
                              -LATRVRMQAVSLATVMLGQGIAFDQQGSELLRSKSFTRDSYDS
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Kishore, Ganesh M.
APPLICANT: Krohn, Bradley M.
TITLE OF INVENTION: No. 5750876el
TITLE OF INVENTION: Containing It
NUMBER OF SEQUENCES: 11
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APPLICATION NUMBER: 1
FILING DATE: 28-JUL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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370 TVYHPQSRKVEQYEVTDP-
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                                                                                                                                                          299 AAEALSYGAQ--LADGGVTFRVWAPTAQQVDVVVYSADKKVIGSHPMTR-----DSASGA 351
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                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
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                                   WSLSLPTSTIKNTYGITGAVYYGYRAWGPNWPYDAAWTKGSATGFVSDVDNAGNRFNPNK 118
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                                                                                                                                                                                                  6.2%; Score 349; DB 1; Length 746; ilarity 22.4%; Pred. No. 7.2e-21; Conservative 101; Mismatches 304; Indels 2
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PCT-US95-09323-11
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CLASSIFICATION:
PRIOR APPLICATION NAMBER: US 08/281902
APPLICATION NUMBER: US 08/281902
FILING DATE: 28-JUL-1994
"INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                         Sequence 11, Application PC/TUS9509323 GENERAL INFORMATION:
                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                               TITLE OF INVENTION: Novel Isoamylase Gene, Compositions TITLE OF INVENTION: Containing It and Methods of Using NUMBER OF SEQUENCES: 11
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                APPLICATION NUMBER: FILING DATE:
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; LENGTH: 746 amino acids
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Best Local Similarity 22.4%;
Matches 199; Conservative 10
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LENGTH: 746 amino acid
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AYNGWSGAVDFKLPWPGTGKQWYRVTDTATWNEGPNAV--ALPGSETL
                                                                                                                   GDGSAVMKRVD-FRNTGSDQQAGLLVMTVDDGMKAGA---SLDSRLDGLVVAINAAPESR 1028
                                                                                                                                                            -NNNTYNL-----DSAANWLYWSR--SALEADHETYTKRLIAFRKAHPALRPANFYSAS
                                                                                                                                                                                                  LQDNNYNVGMPRISDDGSNYEVITRVKEMVATPGEAELKOMTAFYQELTELRKSSPLFTL
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APPLICATION NUMBER: 224,114
FILING DATE: 25-JUL-1988
SEQ ID NO:3:
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FILING DATE: 08-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 749,621
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CURRENT APPLICATION DATA:
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YSWDQGMSAGTGAAVNQRRAARTGMAFEMLSAGTPLMQGGDEYLRTLQCNNNAYNLDSSA 60:
                                                                                                                                              --DFSGSSNLFQSSGRSPWNSINFIDVHDGMTLKDVYSCNGANNSQAWPYGPSDGGTSTN
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RESULT 14
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APPLICANT: TOCNONI, ANGELO;CARRERA, PAOLO;CAMERINI, BARBARA;
;GALLI, GIULIANO;LUCCHESE, GIUSEPPE;GRANDI, GUIDO;DI GENNARO, CARLA
TIPLE OF INVENTION: CLONING OF THE GENE CODING THE ISOAMYLASE
; ENZYME AND ITS USE IN THE PRODUCTION OF SAID ENZYME
; NUMBER OF SEQUENCES: 7
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CURRENT APPLICATION NUMBER: US/08/1,797
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FILING DATE: 08-JAN-1993
PRIOR APPLICATION DATA:
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                                    -DALRONOGIGSGAGVLPNELASLSDDQVRHLADLTRLGMAGNLADFVMIDKDGAAKKGS 816
                                                                          FDAADSNVAIN-RILREFTVRPAAGGSGLDLFAEPWAIGGNSYQLGG-FPQGWSEWNGLF
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	80 ATDPEGTTRIKEERTMIQAIKQDLGMNVIMDVVYNHTNAAGPTDRTSVLDKIVPWYY 636 	Оу 58 Db 25	
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	*** UTAGDSNNVQHLKTLSASGVTHVEILPVFDLATVNEFSDKVADIQQPFSRLCEVNSAVKS 519	ОУ 460 Db 199 OУ 520	
	169 MTVYHPQSRKVEQYEVTDPYAHSLSTNSEYSQVVDLNDSA 408	ОУ 36 Db 8	
	311 DG-GVTFRVWAPTAQQVDVVVYSADKKVIGSHPMTRDSASG-AWSWQGGSDLKGAFYRYA 368 	Фу 3:	
32;	Query Match 5.7%; Score 319.5; DB 3; Length 726; Best Local Similarity 22.2%; Pred. No. 2.2e-18; Matches 160; Conservative 88; Mismatches 219; Indels 253; Gaps	Query Best I Match	
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	IER APPLICATION NUMBER: 0787/97 IER PILING DATE: 1997-07-02 IER APPLICATION NUMBER: 60/055,867		
	REFERENCE: 5262.204-US ENT APPLICATION NUMBER: US/09/129,075 ENT FILING DATE: 1998-08-04		
	ANT: Tsutsumi, No. 60871491ko ANT: Bisgard-Frantzen, Henrik ANT: Svendsen, Allan		
	SULT 15 -09-129-075-4 Patence 4, Application US/09129075 Patent No. 6087149 GENERAL INFORMATION:	∞ ≅	
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                                                                                                                                          364 LARELYDVDMLSTFFQVIQQDPVLSQVKLIAEPWD------VGPGGYQYGHFPW 411
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Search completed: April 22, 2001, 09:05:59 Job time: 4043 sec

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Copyright
GenCore version (c) 1993 - 2000
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Š protein protein search, using sw model

Run

April 22, 2001, 09:04:38; Search time 62.87 Seconds (without alignments) 1192.568 Million cell updates/sec

Title: Perfect score: US-09-262-126C-4 5633 1 MLRYTRNALVLGSL

Sequence: MLRYTRNALVLGSLVLLSGC...... .AVLELPQGEAQGAGLPVSSK 1091

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:

198801 seqs, 68722935 residues

Total number of hits satisfying chosen parameters: 198801

Minimum Maximum DB DB seq length: length: 0 20000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 s

summaries

Database

PIR_67:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

alpha-dextrin endo-1,6-alpha-glucosidase (EC 3.2.1.41) precursor - Klebsiell N;Alternate names: pulluianase C;Specites: Klebsiella pneumoniae C;Date: 13-Jan-1995 *sequence_revision 13-Jan-1995 *text_change 08-Oct-1999 C;Accession: S1183; A32880 R;Kornacker, M.G.; Pugaley, A.P. Mol. Microbiol. 4, 73-85, 1990 Klebsiella pneumon

A; Title: Molecular characterization of pulA and its product, pullulanase, A; Reference number: S11823; MUID:90205629
A; Accession: S11823 a secreted

A; Status: preliminary

A; Molecule type: DNA
A; Residues: 1-1090 KKOP>
A; Residues: 1-1090 KKOP>
A; Cross references: EMBL: X52181; NID: 943912; PIDN: CAA36431.1; PID: 943913
A; Cross references: EMBL: X52181; NID: 943912; PIDN: CAA36431.1; PID: 943913
A; D'Enfert, C.; Pugsley, A.P.
J. Bacteriol. 171, 3673-3679, 1989
J. Bacteriol. 171, 3673-3679, 1989

A;Title: Klebsiella pneumoniae pulS gene encodes an outer membrane lipoprotein requir A;Reference number: A32880; MUID:89291709
A;Accession: A32880

A;Status: preliminary A;Molecule type: DNA A;Residues: 944-1090 <DEN>

A;Cross-references: GB:M29097; NID:g342046; PIDN:AAA61976.1; PID:g643577 C;Keywords: glycosidase; hydrolase; polysaccharide degradation

οy δÃ Qy Д Q 멍 . p В ₽ Qy Query Match Best Local S Matches 1090; 181 240 241 180 120 121 60 61 Local Similarity SMREPHLSSYAAFKLPDNANVDELLQGETVAIAAAEDGILISATQVQTAGVLDDAYAEAA 300 Conservative 99.78; Score 5618.5; Pred. No. 0; 0; Mismatches 0; DΒ 0: 2 Indels Length 1090; : Gaps 239 240 ;

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RESULT 2
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A19ha-dextrin endo-1,6-alpha-glucosidase (EC 3.2.1
N.Alternate names: pullulan 6-glucanohydrolase; pu
C;Species: Klebsicila pneumoniae
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988
C;Accession: A26879; 802472
R;Katsuragi, N.; Takizawa, N.; Murooka, Y.
J. Bacteriol. 169, 2301-2306, 1987
A;Title: Entire nucleotide sequence of the pullulan
A;Reference number: A26879; MUID:87194626
A;Note: K. aerogenes
A;Accession: A26879
A;Molecule type: DNA
A;Residucs: 1-1096 <KAT>
A;Experimental source: strain W70
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IGSGAGVLPNELASLSDDQVRHLADLTRLGMAGNLADFVMIDKDGAAKKGSEIDYNGAPG
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R;Charalambous, B.M.; Keen, J.N.; M
EMBO J. 7, 2903-2999, 1988
A;Title: Collagen-11ke sequences st
A;Reference number: S02472; MUID:89
A;Accession: S02472
A;Status: not compared with concept
A;Molecule type: DNA
A;Residues: 1-74 <CHA>
A;Note: part of this sequence was c
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RESULT 3

$38801

alpha-dextrin endo-1,6-alpha-glucosidase (EC 3.2.1.41)

alpha-dextrin endo-1,6-alpha-glucosidase (EC 3.2.1.41)

N;Alternate names: pullulanase
C;Species: Klebsiella pneumoniae
A;Variety: ATCC 15050; strain K21
C;Date: 07-Apr-1994 *sequence_revision 07-Apr-1994 *tc
C;Accession: $38801; A25025; $04864
R;Janse, B.J.H.; Steyn, A.J.C.; Pretorius, I.S.
Curr. Genet 24, 400-407, 1993
A;Title: Regional sequence homologies in starch-degrac
A;Reference number: $38801; MUID:94130317
A;Accession: $38801
A;Accession: $38801
A;Accession: $38801
A;Accession: $38801
A;Accession: $1-1038 <JAN>
A;Cross-references: EMBL;L19312
A;Experimental source: ATCC 15050
R;Chapon, C.; Raibaud, O.
J. Bacteriol: 164, 639-645, 1995
A;Title: Structure of two divergent promoters located
A;Reference number: A91807; MUID:86033621
A;Accession: A25025
A;Accession: A25025
                                                                                                                                                                                                                                  A:Title: Klebsiella pneumoniae strain K21:
A:Reference number: S04864; MUID:89343636
A:Accession: S04864
A:Molecule type: protein
A:Residues: 'X', 21-31,'X', 33,'X' <KOR>
A:Experimental source: strain K21
C:Genetics:
                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-65 <CHA>
A; Residues: 1-65 <CHA>
A; Cross-references: GB.M12503; NID:g149223;
A; Cross-references: GB.M2503; NID:g149223;
R; Kornacker, M.G.; Boyd, A.; Pugsley, A.P.;
Mol. Microbiol. 3, 497-503, 1989
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                                                                                                                                                                   A;Gene: pulA
C;Keywords: glycosidase; hydrolase; lipoprotein; polysaccharide
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-1038/Product: pullulanase #status experimental <MAT>
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                                                MLRYTRNALVLGSLVLLSGCDNGSSSSSSSGNPD---TPDNQDVVVRLPDVAVPGEAVTA 57
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   VENQAVIHLVDIAGITSSSAADYSSKNLYLWNNETCDALSAPVADWNDVSTTPSGSDKYG
                                  MLRYTCNALFLGSLILLSGCDN-SSSSSSSSSSDNPGNPDNQDVVVRLPDVAVPGEAVMA
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83.3%;
                                                                                             Score 4435.5;
Pred. No. 5.6e
52; Mismatches
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Plastow, G.S.
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C;Species: Spinacia c
C;Date: 07-May-1995 #
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#sequence_revision
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   01-Sep-1995 #text_change
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09-Sep-1997

891 891 831 831 771 775 717

657 598 597 538 537 478

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C;Accession: S51324
R;Kenz, A.; Schmid, R.; Kossmann, J.; Beck, E.
submitted to the EMBL Data Library, January 1995
A;Description: Sequence of a cDNA of the Spinacia oleracea L. starch debranching enzyme.
A;Reference number: S51324
A;Accession: S51324
A;Status: preliminary
A;Kolocule type: mRNA
A;Residues: 1-964 <REN>
A;Cross-references: EMBL:X83969; NID:g634092; PID:g634093
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   GMPRISDDGSNYEVITRVKEMVATPG-EAELKQMTAFYQELT---ELRKSSPLFTLGDGS
                                                    ATRVRMQAVSLATVMLGQGIAFDQQGSELLRSKSFTRDSYDSGDWFNRVDYSLQDNNYNV
                                                                                                                                                                                                                                                                                                                                                                                   LQLPGVIDELY-----SYDGPLGAVFSENTISLYLWAPTAQAVSASIF----KDPSGGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALAEAHWVDKNTLLW----PGGQDKPIVRLYYSHSSKVAADGEGKFTDR------YLKL 231
                                      DERCRYNHLATSILALSQGIPFFHAGDELLRSKSLDRDSYNSGDWFNRLDFSYNSNNWGV
                                                                                                     DYILTNCDGKQVKGSEVYTYGGTPVGYAMQPTETINYVSAHDNETLFDIVSLKTPTYTTV
                                                                                                                                       DFVMIDKDGAAKKGSEI-DYNGAPGGYAADPTEVVNYVSKHDNQTLWDMISYKASQEADL
                                                                                                                                                                          DAVLGGGPF--GPPLQ--QGYVTGLSLQPNDHDHSGKANADRMLAVAKDHIQVGMAGNLR
                                                                                                                                                                                                           DSVRGGGPFDSGDALRQNQGTGSGAGVLPNE---LASLSDDQVRHLA-DLTRLGMAGNLA
                                                                                                                                                                                                                                               KATNMLQGLSKNIDGVEGSSIYLYGEGWDFGEVANNARGVNASQLNLGGTGIGSFNDRIR
                                                                                                                                                                                                                                                                        SAWERIKALNPD-----IYFFGEGWDSNQ---SDRFEIASQINLKGTGIGTFSDRLR 745
                                                                                                                                                                                                                                                                                                                    LR-RDNDGATENSTCVNDTASEHFMVERLILDDLKHWAVNYKVDGFRFDLMGHIMKHTMV
                                                                                                                                                                                                                                                                                                                                      QRLNETTGSVESATCCSDSAPEHRMFAKLIADSLAVWTTDYKIDGFRFDLMGYHPKAQIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          -KKWKF-----VDTKRFETLPPDSEEQQAQITAIRDEDGYNWGYNPVLWGTPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VKSSEFAGYCDSGSTVEEVLNQLKQSDSQDNPQVQALNTLVAQTDSYNWGYDPFHYTVPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YLAFTSQDSAGVNHLEKLSAAGLTHVHLLPSFQFAEVDD--DK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YLALTAGDSNMYQHLKTLSASGYTHYELLPYFDLATVNEFSDKVADIQQPFSRLCEVNSA 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TLLADLSSETLKPEGWENLADEKPHLLSP----SDISLYELHIRDFSAYDLTVHPDLRGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SQVVDLNDSALKPDGWDNLT---MPHAQKTKADLAKMTIHESH1RDLSAWDQTVPAELRGK 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLQTVQLIESNGVWSAVGPRTWEGCYYVYEITVYHHSTLRIEKSFAIDPYARGISADVKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PMTR---DSASGAWSWOGGSDLKGAFYRYAMTVYHPQSRKVEQYEVTDPYAHSLSTNSEY 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VQTAGVLDDAYAEAAEALSY----GAQLADGGVTFRVWAPTAQQVDVVVYSADKKVIGSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NSCRAYWPSKYTFAWNVDIGNGS-----YYLFASKTAA---LKFTDAGIEGYDVKIKL
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Pred. No. 4.2e-83;
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starch debranching enzyme, pullulanase-type - maize
C;Species: Zea mays (maize)
C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 29-Oct-1999
C;Accession: T01688
C;Accession: T01688
R;Beatty, M.K.; Rahman, A.; Cao, H.; Woodman, W.; Lee, M.; Myers, A.M.; James, M.G.
Plant Physiol. 119, 255-266, 1999
A;Title: Purification and molecular genetic characterization of ZPU1, a pullulanase-t
A;Reference number: Z14395; MUID:99097061
A;Accession: T01688
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-962 <BEA>
A;Cross-references: EMBL:AF080567; NID:g3411265; PIDN:AAD11599.1; PID:g3411266
A;Experimental source: endosperm
C;Genetics:
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C; Function:
A; Description:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GVALAE-----AHWVDKNTLLWPGGQDKPIVRLYYSHSSKVAADGEG-KFTDRYL
                                                                                                                                                                                                                                  GDSNMYQHLKTLSASGYTHYELLPYFDLATVNEFSDKVADIQQPFSRLCEVNSAVKSSEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAGVLDDAYAEAAEALSYGAQLADGGVTFRVWAPTAQQVDVVVYSADKKVIGSHPMTR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GVAVAESAQGFILDARAYWVTKSLIAWNISDQKTSLFLYASRNATMCMSSQDMKGYDSKV 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLPPKDHNESNWPLI---KKRLANPSYKPDKNHIIAAVENFTNLLQIRYSSPLFRLRSAK
                                                                                                                                                                                                                                                                                                              LNDSALKPDGWDNLTMPHAQKTKAD-LAKMTIHESHIRDLSAWDQTVPAELRGKYLALTA 462
                                                                                                                                                                                                                                                                                                                                                                                                                                        LPGVLDDMFAYTG----PLGTIFSEEAVSMYLWAPTAQDVSVSFYDGP-----AGPLLETV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KLTPTT--VSQQVSMRFPHLSSYAAFKLPDNANVDELLQGETVAIAAAEDGILISATQVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PDLRAKSLQLHPVQSTSGDTVVKESKYEPSTGCFTIPPKSTAVFVEPR
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                 ETTGSVESATCCSDSAPEHRMFAKLIADSLAVWTTDYKIDGFRFDLMGYHPKAQILSAWE
                                                                                       QLNELNGVWSVTGPRNWENRYYLYEVTVYHQTTGNIEKCLAADPYARGLSANSTRTWLVD
                                                                                                                                                                                                                                                                                                                                                                                         --DSASGAWSWQGGSDLKGAFYRYAMTVYHPQSRKVEQYEVTDPYAHSLSTNSEYSQVVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELQPENDGLPSSVTQKFPFISSYRAFRIPSSVDVATLVKCQLAVASFDAHGNRQDVTGLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -EFAGETLOLSAIOQTAGENSLANGVQIAADGTVTLPAWSVAVLELPQ 1078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DIEDRYRFHNNYPSWIPGLIAMSIEDG-HAGAPGLSQIDPKFQYIVVIINYQPTETKFYN
DSNGQTENSAAVNNTASEHFMYDRLIVDDLLNWAVNYKVDGFRFDLMGHIMKKTMIRAKS
                                                                  SNPDGPSRIIEYRLMVQALNR-LGLRVVMDVVYNHLYSSGPFAITSVLDKIVPGYYLR-R
                                                                                                                                           ----NWKCVDEIELSKLPPGSDLQ-----QAAIVAIQEEDPYNWGYNPVVWGVPKGSYA
                                                                                                                                                                             AGYCDSGSTVEEV-LNQLKQ-SDSQDNPQVQALNTLVAQTDSYNWGYDPFHYTVPEGSYA
                                                                                                                                                                                                                   QDSVGIEHLKKLSDAGLTHVHLLPSFQFGGVDD------IKS---
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probable alpha-dextrin endo-1,6-alpha-glucosidase (EC
N;Alternate names: pullulanase
C:Species: Hordeum vulgare (barley)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #te
C:Accession: T04377
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A;Residues: 1-904 <LOK>
A;Cross-references: EMBL:AF022725; NID:g2502057; PIDN:AAD04189.1; PID:g2677837
A;Experimental source: cv. Igri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, December 1997
A;Description: Isolation and characterization of starch debranching enzyme, limit dextra;Reference number: Z15320
A;Accession: T04377
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A;Introns: 21/3; 70/1; 87/3; 124/1; 169/3; 235/2; 285/2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R; Lok,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary; translated
                                                                                                                                                                                                                                                                       Query Match 25.3%; S
Best Local Similarity 35.7%; P
Matches 330; Conservative 176;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .; Kristensen, M.; Planchot, V.; Leah, R.; Svendsen, d to the EMBL Data Library, December 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RIKALNPD------IYFFGEGWDSN---QSDRFEIASQINLKGTGIGTFSDRLRDSVR 749
                                                                                                                                                        QVSMRFPHLSSYAAFKLFDNANVDELLQGETVAIAAAEDGILISATQVQTAGVLDDAYAE 298
                                                                                                                                                                                                  ARAYWYTSDLIAWNYGELEAQSYCLYASRAAAMSLSPSNGGIQGYDSKYELQPESAGLPE 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FHNTGPSLVPGVIVMSIEDARNDRHDMAQIDETFSCVVTVFNVCPYEVSIEIPDLASLRL
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                                                                                                                                                                                                                                      AEAHWVDKNTLLWPGGQ-DKPIVRLYYSHSSKVA---ADGEGKFTDRYLKLTPTT--VSQ 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QLHPVQVNSSDALARQSAYDTATGRFTVPKRTAAVFVEPR 961
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EWENRYYLYEVDVYHPTKAQVLKCLAGDPYARSLSANGARTWLVDINNETLKPASWDELA
                               DLKGAFYRYAMTVYHPQSRKVEQYEVTDPYAHSLSTNSEYSQVVDLNDSALKPDGWDNLT 418
                                                                                                 AAEALSYGAQLADGGVTFRVWAPTAQQVDVVVYSADKKVIGSHPMTRDSASGAWSWQGGS 358
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35.7%; Pred. No. 2.2e-
tive 176; Mismatches
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S; Smith, H.O.; Venter, J.C. Science 286, 1571-1577, 1999 A;Title: Genome sequence of t A;Reference number: A73250; MA;Accession: D75524
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R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dx, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zale S; Smith, H.O.; Venter, J.C.; Fraser, C.M.
A; Cross-references: GB: AE001900;
A; Experimental source: strain R1
                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-910 <WHI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IAADCTVTLPAWSVAV 1073
                                                                             --LSGGVSATNPYRDLLVIFNGSADAVTLNDASASGMKLHPVLAASSDPIVRTSKVSGTQ
                                                                                                  DGMKAGASLDSRLDGLVVAINAAPESRTLNEFAGETLOLSAIQQTAGE----NSLANGVQ
                                                                                                                                                                          AGDELLRSKSFDTDSYNSGDWFNALDWTGHTNGFGKGLPPAEKNEANWALYRTLLGDAAL
                                                                                                                                                                                                                                       GGYÄADPTEVVNYVSKHDNOTLWDMISYKASQEADLATRVRMQAVSLATVMLGQGIAFDQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       •VALAEAHWVDKNTLLWPGGQDKPIVRLYYSHSS--KVAADGEGKFTDRYLKLTPTTVSQ
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                                                                                                                              KVTP--ADITRASDHERELLRVRSSSSLERLDTAAQVQQSLSE----LPAPTGYIAMK--
                                                                                                                                                                                                QCSELLRSKSFTRDSYDSGDWFNRVDYSLQDNNYNVGMPRISDDGSN---YEVITRVKEM
                                                                                                                                                                                                                        AGYAASPRETINYASAHDNOTLWDAVILKTPANMNSAARVRFQNLAHSYLLIGQGLPFVP
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                                                                                                                                                                                                                                                                                                                     IYLYGEGWDFGEVQGNRRGANATQLNLYGAGIGTFNDRVRDALRGGSPFGG----LQEQG
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                                  ASVPALTTAV
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      NGYYQGNEADTRRELATYADHIQIGLAGNLKDYVLRTHTGEAKKGSDIYTFDGSPVGYTS
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T03760

alpha-dextrin endo-1,6-alpha-glucosidase (EC 3.2.1.41) - rice

N;Alternate names: pullulanase

C;Species: Oryza sativa (rice)

C;Date: 23-Apr 1999 #sequence_revision 23-Apr-1999 #text_change 21-Jul-2000

C;Accession: T03760

C;Acces
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A;Accession: T03760
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-986 < NAK>
A;Cross-references: EMBL:D50602; NID:g836661; PIDN:BAA09167.1; PID:g1783306
A;Experimental source: cv. Fujihikari, endosperm
C;Genetics:
A;Map position: 4
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
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Best Local Similarity
Matches 333; Conserv
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                                                                                                                                                                                                                                                                                                                                                                             IADSLAVWTTDYKIDGFRFDLMGYHPKAQILSAWERIKALNPD-----IYFFGEGWD
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                                                                                                                                                                                                                                                                                  TVDDLLNWAINYKVDGFRFDLMGHIMKSTMIRAKSAIRSLTRDVHGVYGSKIYLYGEGWD
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NELASLSDDQVRH----LADLTRLGMAGNLADFVMIDKDGAAKKGSEI-DYNGAPGGYAA
                                                                                                FGEVAQNKRGINASQINMSGTGIGSFNDRIRDSVNGGNPF--GNPLQ--QGFSTGLFLEP
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Mismatches
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1.2e-72;
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A;Molecule type: DNA
A;Residues: 1-843 <ARNY
A;Residues: 1-843 <ARNY
A;Cross-references: GB:AE001821; GB:AE000512; NID:g4982421; PIDN:AAD36907.1;
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM1845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pullulanase - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: H72204
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft,
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Ri
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                                                                                                                                              AYAEAAEALSYGAQLADGGVTFRVWAPTAQQVDVVVYSADKKVIGSHPMTRD-SASGAWS
                                                                                                                                                                                                                                                                                                                                           VAVVKLPMDLTKVGIIVRLNEWQAKDVAKDRFIEIKDG---KAEVWILQGVEEIFYEKPD
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                                                                                                                                                                                                  DID-----VTNYVRIVLSESLKEEDLRKDVELIIEGYKPARVIMME-----ILDD
                                                                                                                                                                                                                               TVSQQVSMRFPHLSSYAAFKLPDNANVDELLQGETVAIAAAEDGILISATQVQTAGVLDD
                                                                                                                                                                                                                                                                                                        AFRAAFGVALAEAHWVDKNTLLWPGGQDKPIVRLYYSHSSKVAADGEGKFTDRYLKLTPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENQAVIHLVDIAGITSSSAADYSSKNLYLWNNETCDALSAPVADWNDVSTTPSGSDKYGP 118
                                                       AVVEGDLDGVFYLY------QLENYGKIRTTVDPYSKAVYANSKKSAVVNL--ART
                                                                                        WQGGSDLKGAFYRYAMTVYHPQSRKVEQY----EVTDPYAHSLSTNSEYSQVVDLNDSAL
                                                                                                                                                                                                                                                                      TSPRIF-FAQARSNKVIEAFLTNPVDTKK------KELFKVTVDGKEIPVSRVEKADPT
                                                                                                                                                                                                                                                                                                                                                                                                             ETTIVVHYHRYDG-----KYDGWNLWIWPVE-----PVSQ-EGKAYQFTGEDDFGK
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                                                                                                                            -ELGAVYSPEKTIFRVWSPVSKWVKVLLFKNGEDTEPYQVVNMEYKGNGVWE
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GTEVIETVEGTIELDPLSAYVL
                              GVQI -- AADGTVTLPAWSVAVL 1074
                                                                                             LIVMTVDDGMKAGASLDSRLDGLVVAINAAPESRTLNEFAGETLQLSAIQQTAGENSLAN 1054
                                                                                                                                                                                             LTSQGVPFLHGGQDFCRTKNF----
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                                                                                                                               -----RKLQFIDVFNYHKGLIKLRKEHPAFRLKNAEEIKKHLEFLPGGRRIVAF
                                                                                                                                                          ITRVKEMVATPGEAELKQMTAFYQELTELRKSSPLFTLGDGSAVMKRVDFRNTGSDQQAG
                                                                                                                                                                                                                          --GQGIAFDQQGSELLRSKSFTRDSYDSGDWFNRVDYSLQDNNYNVGMPRISDDGSNYEV 934
                                                                                                                                                                                                                                                         YDGKLIKSFALDPEETINYAACHDNHTLWDKNYLAAKADKKKEWTEEELKNAQKLAGAIL
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                                                               -KDHAGGDPWKD-IVVIYNGNLEK-----TTYKLPEGKWNVVVNSQKA 818
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RESULT 10
G69585
pullulanase amyX - Bacillus subtilis
C:Species: Bacillus subtilis
C:Species: D3-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
C:Accession: G69585
C:Accession: G69585
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
Nature 390, 249-256, 1997
A.; Ehrlich, S.D.; Eritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino
A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Lin, H.; Masuda, S.; Mau
y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl
A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya
T.; Winters, P.; Wipat, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya
T.; Winters, P.; Wipat, A.; Tanaka, T.; Yanamoto, H.; Yanamoto, K.; Yata, K.; Yoshida
A; Noteviele type: DNA
A; Residues: 1-718 <KUN>

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RESULT 11
A84112
Alkaline amylopullulanase BH3697 [imported] -
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-
C;Accession: A84112
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les 224; Conserv
                                                                                                                                  LPNDIPYRLLCDPSGFQEDPTEIKKTVAVNGI-----
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               01-Dec-2000 #text_change
                                              Bacillus halodurans (strain C-125)
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R:Takami, H.; Nakasone, K.; Takaki, Y.; Macno, G.; Sasaki, R.; Mucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium A; Reference number: A83650; MUID:20263314
A:Accession: A84112
A:Status: preliminary
A; Molecule type: DNA
A:Residues: 1-1072 <STO>
A; Cross-references: GB:AP001519; GB:BA000004; NID:g10176109; PID A; Experimental source: strain C-125
C:Genetics:
A;Gene: BH3697
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Best Local Similarity 23.3
Matches 262; Conservative
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   QINLKGT-GIGTFSDRLRDSVRGGGPFDSGDALRQNQGIGSGAGVLPNELASLSDDQVRH 787
                                                                         WTTDYKIDGFRFDLMGYHPKAQILSAWERIKALNPDIYFFGEGWDSNQSDR----FEIAS
                                                                                                             YNHTAA-----VEIFEDLMPNYYHFM-DADGTPRTSFGGGRLGTTHKMSRRILVDSITY
                                                                                                                                                 YNHTNAAGPTDRTSVLDKIVPWYYQRLNETTGSVESATCCSDSAPEHRMFAKLIADSLAV
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                                       WVEEYKVDGFRFDMMGDHDAETIQIAYDRAKELNPNIVMIGEGWRTYVGDEHGGDIMPAD
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QDWMQHTESVGVFSDEFRNELK

SEGOPRE

Qy 400 QVVDLNDSALKPDGWDNLTMPHAQKTKADLAKMTIHESHIRDLSAWDQTVPAELRGKYLA 459 200 VIFDLKRTDAASWPTVHPIPPEHTIIYELHIRDATVYPGS-GHHKKGTYLS 249 Qy 460 LTAGDSNMVGHLKTLSASGVTHVELLPVFDLATVNEFSDKVADIQQPFSRLCE 512	Query Match 10.5%; Score 593.5; DB 2; Length 717; Best Local Similarity 26.1%; Pred. No. 3.9e-28; Matches 203; Conservative 99; Mismatches 290; Indels 1B7; Gaps 28; Qy 280 LISATQVOTAGVLDDAYAEAAEALSYGAOLADGGVTERVMAPTAGQVDVVYSADKKVIG 339	RESULT 12 H84057 pullulanase amyX [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000 C;Accession: H84057 R;Takami, H; Nakasone, K; Takaki, Y; Maeno, G; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000 A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Accession: H84057 A;Ccession: H84057 A;Ccession: H84057 A;Ccession: H84057 A;Residues: 1-717 <sto> A;Residues: 1-717 <sto> A;Experimental source: strain C-125 C;Genetics: A;Gene: amyX A;Gene: amyX</sto></sto>	OY 788 LADLTRLGMAGNLADFVMIDKDGAAKKGSEIDYNGAPGGY-AADPTEVVNYVSKHDNQ 844 1
25 366 81 418 139 463 199 523	n lait illinite	Oy 975 GSAVMKRVDFRNTGSDQQAGLLVMTVDDGMKAGASLDSRLDGLVVAIN 1022	Oy 692 KAQILSAWERIKALNPDIYFFGEGWDSNQSDRFEIASQINLKGTGIGTFSDRLR 745

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probable gigX protein - Mycobacterium tuberculosis (strain H37RV)

C;Secles: Mycobacterium tuberculosis

C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000

C;Accession: A70764

C;Ole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Dieviln, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Rajundream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Rajundream, R. Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A; Feference number: A70500; MUID:98295987

A;Accession: A70500; MUID:98295987

A;Accession: A70500; MUID:98295987

A;Cross-references: GB:Z74020; GB:AL123456; NID:g3261584; PIDN:CAA98327.1; PID:g1403478
A;Esperimental source: strain H37Rv
C;Genctics:
A;Gene: gigx
C;Superfamily: glyx protein
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AYPLGATYDGAGTNFSLFSEIAEKVELCLIDED-GVESRIPL--DEVDG-YVWHAYLPNI 79
                                         ALSYGAQLADGGVTFRVWAPTAQQVDVVVYSADKKVIGSHPMTRDSASGAWSWQGGSDLK 361
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                                                                                6.3%; Score 352.5; DB 2; Length 22.8%; Pred. No. 1.7e-13; ative 113; Mismatches 294; Indels
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GDIDLTVTATDTFSVPARSLLVL
                                    -----QIAADGTVTLPAWSVAVL 1074
                                                                                  CVAVFLNGEAITAPDARGERVVDDSFLLCFNAHDHDVEFVMPHDGYAQQWTGELDTNDPV
                                                                                                                              YVAINAAPESRTLNEFAGETLQLSAI-----
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                                                                                                                                                                         KNHKVFRRRFFEGEPIRSGDEVRDIAWLTPSGRE-----MTHEDW----GRGFDR-----
                                                                                                                                                                                                                 KSSPLF---TLGDGSAVMKRVDFRN----TGSDQQAGLLVMTVDDGMKAGASLDSRLDGL 101;
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A;Title: Genome sequence of t: A;Reference number: A75250; M A;Accession: B75540 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-720 <WHI> glycogen operon protein GlgX - Delnococcus radiodurans (strain R1)
c;Species: Delnococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C;Accession: B75540
C;Accession: B7540
C;Acc RESULT B75540 the radioresistant bacterium MUID: 20036896 Deinococcus J.D.; Dodson, T.; Zalewski, radiodurans

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A;Cross references: GB:AE001888; GB:AE000513; NID:g6457936; PIDN:AAF09848.1; PID:g645793 A;Experimental source: strain R1 C;Genetics: A;Gene: DR0264 A;Map position: 1 C;Superfamily: glyx protein Ş 멍 밁 Ϋ́ 밁 Qy В Ş 밁 δ 밁 Ş B δô 밁 Š Ъ Ş 밁 Ş 밁 2 밁 Ş 뮹 8 밁 S Вb S Ş Ouery Match 6.1%; Score 344.5; DB 2; Length 720; Best Local Similarity 21.8%; Pred. No. 5e-13; Matches 198; Conservative 113; Mismatches 270; Indels 327; Gaps Query Match Best Local Similarity 1083 GAGLPVSS 1090 1025 PESRTLNEFAGETLQLSAIQQTAGENSLANGVQIAADGTVTLPAWSVAV--LELPQGEAQ 1082 417 LTMPHAQKTKADLA------KMTIHESHIRDLSAWDQTVPAELRGK 456 663 PDLGGCGEW---DLLLDTSDDGAEE-----KVAAGGETTLRGRSVKLYRCQVPEKELE 712 978 VMKRVDFRNTGSDQQAGLLVMTVDDGMKAGASLDSR-----LDGLVVAINAA------ 1024 557 939 KEMVATPGEAELKOMTAFYQELTELRKSSP-----LFTLG-------DGSA 977 525 879 GIAFDQQGSELLRSKSFTRDSYDSGDWFNRVDYSLQDNNYNVGMPRISDDGSNYEVITRV 938 847 WDMISY----KASQEAD------LATRYRMQAVS--LATVMLGQ 878 437 734 GTGIGTF-----SDRLRDSVRGGGPFDSGDALRQNQGIGSGAGVLPNELASLSDDQVR 786 349 FRFDLASTLARGLHEVDQ-LSGFFTIIHQDPIISQVKLIAEPWDVGEG------ 395 297 DN--PTYYRLVADDQRFYFDYTGTGNSLNV-----RHPQTLQLIMDSLRYWVTEMHVDG 348 529 DKIVPWYYQRLNET-----TGSVESATCCSDSAPEHRMFAKLIADSLAVWTTDYKIDG 681 517 VKSSEFAGYCDSGSTVEEVLNQLKQSDSQDNPQVQALNTLVAQTDSYNWGYDPFHYTVPE 576 185 YAGVAT--PAILDYLRDL---GITAIEFLPVHQ------HVDDPF-----457 YLALTAGDSNMVQHLKTLSASGVTHVELLPVFDLATVNEFSDKVADIQQPFSRLCEVNSA 516 362 GAFYRYAMTV---YHPQS--RKVEQYEVTDPYAHSLSTNSEYSQVVDLNDSALKPDGWDN 416 306 GAQLADGGVTFRVWAPTAQQVDVVVYSADKKVIGSH----PMTRDSASGAWSWQGGSDLK 361 465 RDSVTYEQKHNEANGEGNNDGHNHNITWNCGVEGPTDDPEINRLRGQQMRNFLATLLLGQ 524 787 HLADLTRLGMAGNLADFYMIDKDGAAKKGSEIDYNGAPGGYAADPTEYVNYVSKHDNQTL 846 396 GYOVGNEPVNWAEWNGIYRDDMR-----682 FRFDL-----MGYHPKAQILSAWERIKALNP---DIYFFGEGWDSNQSDRFEIASQINLK 733 69 QPGQRYGYRVHGEYAPEKGLRFNPNVVLLDPYAKALDGTEQFDRGV----FGYVAGGEDD 124 17 GATWDGKGTNFALYSENATGVELCLFDAE-----GHETRFPLTEQT----AFVWHGYLPGI 68 GSSDL------REPYASINFVTAHDGFTL 464 SQMQEEEQRGAPLGLVVDPMFNWVGDQKPGIPFHQSVIYEAHVKGLTMTHPDVPEELRGT 184 EMSDEDWNN----PQTQSLGMFLAGDGL---ADVDAEGKPLTDDHLLLLLSSSYVDLPFKM 662 -----WEKVDEELLAFTRKLIALRKAHPSLHRRKFFAGRNIRGEDVRDIVWLRFDG-A 608 GTPMILGGDEFGRTQGGNNNAY----- 556 -----SFWKGEGGLASEIGY----RIT 436 ----NY-WGYSTLNFFAPD 239 218 45;

Db 713 KLAEPAEA 720

Search completed: April 22, 2001, 09:04:57 Job time: 4138 sec

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Run on:
                                                                                                              OM protein - protein search, using sw model
April 22, 2001, 09:11:53; Search time 52:01 Seconds (without alignments) 718.568 Million cell updates/sec
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Title: Perfect score: Sequence: US-09-262-126C-4 5633 1 MLRYTRNALVLGSLV

MLRYTRNALVLGSLVLLSGC.....AVLELPQGEAQGAGLPVSSK 1091

Scoring table:

Searched: 93435 seqs, 34255486 residues BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). EMBL; X52181; CAA36431.1; EMBL; M12503; AAA25087.2;	"Structure of two divergent promoters located in front of the gene encoding pullulanase in Klebsiella pneumoniae and positively regulated by the malr product.; J. Bacteriol. 164:639-645(1985). [3] SEQUENCE OF 944-1090 FROM N.A. MEDLINE-89291709; PubMed-2661532; D'Enfert C., Pugsley A.P.; "Klebsiella pneumoniae puls gene encodes an outer membrane lipoprotein required for pullulanase secretion."; J. Bacteriol. 171:3673-3679(1989). -I- CATALYTIC ACTIVITY: STARCH-DEBRANCHING ENZYME, HYDROLYSES (1-6)-ALPHA-GLUCOSIDIC LINKAGES IN PULLULAN AND STARCH TO FORM MALTOTRIOSE. -I- SUBCULULAR LOCATION: ATTACHED TO THE MEMBRANE BY A LIPID ANCHOR (PROBABLE). -I- SUBCULULAR LOCATION: ATTACHED TO THE MEMBRANE BY A LIPID ANCHOR (PROBABLE). -I- SUMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.	nd its product, pulluiae UNF5023.";	1 5

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S11823; S11823
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                            QDLGMNVIMDVVYNHTNAAGPTDRTSVLDKIVPWYYQRLNETTGSVESATCCSDSAPEHR
                                                                            HAQKTKADLAKMTIHESHIRDLSAWDQTVPAELRCKYLALTAGDSNMVQHLKTLSASGVT
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N-ACYL DIGLYCERIDE:
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C IN REF: 2):
V-> F (IN REF: 2):
V-> I (IN REF: 2):
V-> S (IN REF: 2):
N-> S (IN REF: 2):
N-> S (IN REF: 2):
D-> DOND (IN REF: 2):
TAVE -> MATA (IN REF: 2):
TAVE -> MATA (IN REF: 2):
MW; 240AE7DFB3FF1BD6 CRC64
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Pred. No. 0;
0; Mismatches
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P07811;
01-AUG-1988
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PULLULANASE
                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                           *Katsuragi N., Takizawa N., Murooka Y.;

*Entire nucleotide sequence of the pullular
aerogenes W70.";

J. Bacteriol. 169:2301-2306(1987).

-I- CATALYTIC ACTIVITY: STARCH-DEBRANCHING
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Katsuragi N., Takizawa N., Murook
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                                                                                                                       (1-6)-ALPHA-GLUCOSIDIC LINKAGES IN PFORM MALTOTRIOSE.

I- SUBUNIT: HOMOTRIMER.

1- SUBCELLULAR LOCATION: ATTACHED TO THANCHOR (PROBABLE).

1- SIMILARITY: BELONGS TO FAMILY 13 OF KNOWN AS THE ALPHA-AMYLASE FAMILY.
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(Rel. 08, Last sequence update)
(Rel. 34, Last annotation updat
PRECURSOR (EC 3.2.1.41) (ALPHA-
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e of the pullulanase gene of Klebsiella
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InterPro; IP
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VGSGAGVLPNELTTI
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                          NPDIYFFGEGWDSNQSDRFEIASQINLKGTGIGTFSDRLRDAVRGGGPFDSGDALRQNQG
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TE; PS00013; PROKAR_LIPOPROTEIN;
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Similarity 84.5%;
34; Conservative
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IPR000461;
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N-ACYL DIGLYCERIDE.

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BY SIMILARITY.
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Pred. No. 1.6e
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C STRAIN-MSBB / DSM 3109;

X MEDIJINE-99287316; PubMed-10360571;

X Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

A Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.

A McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M. McDonald L., Utterback T.R., Malek J.A., Linher K.D., Richardson A McDonald L., Sutton M.D., Pratt M.S., Phillips C.A., Richardson A Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White A Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White A Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;

T "Evidence for lateral gene transfer between Archaea and Bacteria genome sequence of Thermotoga maritima.";

L Nature 399:323-329(1999).

Nature 399:323-329(1999).
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033840;
30-MAY-2000
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                                                                                                This SWISS-PROT entry is copyright. It is produced between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are r
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STRAIN-MSB8 / DSM 3109;
STRAIN-MSB8 / DSM 3109;
MEDLINE-98115241; PubMed-9453151;
Bibel M., Brettl C., Gosslar U., Kriegshaeuser G., Liebl
"Isolation and analysis of genes for amylolytic enzymes
"Isolation and analysis of genes for amylolytic enzymes
hyperthermophilic bacterium Thermotoga maritima.";
FEMS Microbiol. Lett. 158:9-15(1998).
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PULA OR TM1845
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Bacteria; Thermotogales;
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                                                                                                                                          SIMILARITY: BELONGS TO FAMILY 13 C
KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                               (1-6)-ALPHA-GLUCOSIDIC FORM MALTOTRIOSE.
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1. 39, Last sequence update,
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ECURSOR (EC 3.2.1.41) (ALPHA-DEXTRIN EN
PULLULAN 6-GLUCANOHYDROLASE).
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Garrett M.M.,
Richardson D.,
J.A., White O.,
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non-profit institutions as long as its content is in and this statement is not removed. Usage by and for requires a license agreement (See http://www.isb-sib.ch) an email to license@isb-sib.ch).

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EMBL; EMBL; TIGR;

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--GQGIAFDQQGSELLRSKSFTRDSYDSGDWFNRVDYSLQDNNYNVGMPRISDDGSNYEV
                                                         YNG-APGGYAADPTEVVNYVSKHDNQTLWD--MISYKASQEADLATRVRMQAVSLATVML
|:| || || :| || :| || :| || :| || :|
                                                                                                                                                                        T-TRIKEFRIMIQAIKQDLGMNVIMDVVYNHTNAAGPIDRISVLDKIVPWYYQRLNEITG
                                                                                                                                                                                                                                                                                                                                               CDSGSTVEEVLNQLKQSDSQDNPQVQALNTLVAQTDSYNWGYDPFHYTVPEGGSYATDPEG
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                                        YDGKLIKSFALDPEETINYAACHDNHTLWDKNYLAAKADKKKEWTEEELKNAQKLAGAIL
                                                                                                                            QGIGSGAGVLPNELASLSDDQVRIILADLTRLGMAGNLADEVM--IDKDGAAKKG--SEID
                                                                                                                                                            IDPTIILYGEPWGGWGAPIRF---GKSDVAGTHVAAFNDEFRDAIRG-------
                                                                                                                                                                                                                 YLNESGCGNVIASERPMMRKFIVDTVTYWVKEYHIDGFRFDQMGLIDKKTMLEVERALHK
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96261 MW;
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RESULT 4
GLGX_MYCTU STANDARD; PRT; 721 AA.
AC 010767;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE GLYCOGEN OPERON PROTEIN GLGX HOMOLOG (EC 3.2.1.-).
GN GLGX OR RY1564C OR MTCY48.01.
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Matches 197
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ACOLE S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,

AGORDON S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,

A Badcock K., Basham D., Brown D., Chilingworth T., Connor R.,

A Badcock K., Basham D., Brown D., Chilingworth T., Connor R.,

A Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,

A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

A Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,

A Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E.,

A Taylor K., Whitehead S., Barrell B.G.;

T Deciphering the biology of Mycobacterium tuberculosis from the

"Deciphering the Biology of Mycobacterium tuberculosis from the

"Complete genome sequence.";

Nature 393:537-544(1998).

"C HINELTERIATY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO

KNOWN AS THE ALPHA-AMYLASE FAMILY: STRONG, TO E.COLI AND
                                                                                                                                                                                                                         EMBL; Z74020; CAA98327.1; -. HSSP; P10342; 1BF2. TubercuList; Rv1564c; -.
                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hydrolase; Glycosidase.
ACT_SITE 362 362
ACT_SITE 470 470
SEQUENCE 721 AA; 810
                                                                                                                                                                                     InterPro; IPR000461; -
Pfam; PF00128; alpha-amylase;
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      197;
  Similarity 22.8%; P
97; Conservative 113;
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                                                                                                       81081 MW;
                       6.3%;
  Score 352.5;
Pred. No. 1.4e
13; Mismatches
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15-DEC-1998 (Rel. 3
15-DEC-1998 (Rel. 3
                                   Bacteria; CFB q
NCBI_TaxID=239;
SEQUENCE FROM N.A MEDLINE-97340931;
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                                                                                      PRECURSOR
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                                                group;
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37,
 PubMed=9197405
                                                                                    Last sequence update)
Last annotation updat
(EC 3.2.1.68).
                                               Flavobacteria;
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Matches 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Krohn B.M., Barry G.F., Kishore G.M.;

"An isoamylase with neutral pH optimum from a Flavobacterium species: cloning, characterization and expression of the iam gene.";

Mol. Gen. Genet. 254:469-478(1997).

-1- PUNCTION: HAS A HIGH RATE OF HYDROLYSIS FOR GLYCOGEN. DOES NOT CLEAVE PULLULAN. HAS A PH OPTIMUM OF 6-7.

-1- CATALYTIC ACTULTY: HYDROLYSIS OF 1.6-ALPHA-D-GLUCOSIDIC BRANCH LINKAGES IN GLYCOGEN, AMYLOPECTIN AND THEIR BETA-LIMITS DEXTRINS.

-1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydrolase; Glycosidase; SIGNAL 1 32
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  754
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                                                                                                                                                       ACALSPAHA-AIDAQQLGARYDAAQANLAFRYYSSRATRVEVFLY---KNPTGSQEVARL 79
                                                                                TREWKAMVKAF-HDAGIKVYIDVVYNHTGEGGPWSGTDGLSVYNLLSFRGLDNPAYYSLS
                                                                                                                                                                                                                                                                       HLKTLSASGVTHVELLPVFDLATVNEFSDKVADIQQPFSRLCEVNSAVKSSEFAGYCDSG
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  FDSG
                          --- NSCQHGCFNFDKNDSGNALNR--IVAELPPRPAAGGAGADLIAEPWAIGGNSYQVGG
                                                     ERIKALNPDIYFFGEGWDSNQSDRFEIASQINLKGTGIGTFSDRLRD--SVRGG---
                                                                                                           NETTGSVESATCCSDSAPEHRMFAKLIADSLAVWTTDYKIDGFRFDLMGYHPKAQILSAW
                                                                                                                                                                                                                            STVEEVLNQLKQSDSQD-NPQVQALNTLVAQTDSYNWGYDPFHYTVPEGSYATDPEGTTR
                                                                                                                                                                                                                                                         KAAALAALGVTAVEFLPV-----
                                                                                                                                                                                                                                                                                                             AADA----TSVGSKPTRA-LKDEVIYEVHVRGLTRNDDSVPAAERGTY------KGAAR
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203; Conservative
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BY SIMILARITY.
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Pred. No. 1.6
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DALRQNQGIGSGAGVLPNELASLSDDQVRHLADLTRLGMAGNLADFV

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01-MAR-1989
15-DEC-1998
15-DEC-1998
                       J. MO1. B101. 281:885-897(1998).

-!- CATALYTIC ACTIVITY: HYDROLYSIS OF 1,6-ALPHA-D-GIJCCOSIDIC BRANCELINKAGES IN GLYCOGEN, AMYLOPECTIN AND THEIR BETA-LIMITS DEXTR.

-!- INDUCTION: BY MALTOSE.

-!- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
MEDLINE=98387895; PubMed=9719642;
Katsuya Y., Mezaki Y., Kubota M., Mats
                                                                                                                                                                                           Amemura A., Fujita M., Futai M.;
"Transcription of the isoamylase gene
amyloderamosa SB-15.";
J. Bacteriol. 171:4320-4325(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSEAY
                                                                                                                                                                                                                                                                                                               Chen J.H., Chen Z.Y., Chow T.Y., Chen J.C., Tan S.T., Hsu W.H.; "Nuclcotide sequence and expression of the isoamylase gene from isoamylase-hyperproducing mutant, Pseudomonas amyloderamosa JD2: Biochim. Blophys. Acta 1087:309-315(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1019
                                                                                                resolution.";
                                                                                                                  "Three-dimensional structure of Pseudomonas isoamylase
                                                                                                                                                                                                                                                       MEDLINE-89327147; PubMed-2753857;
                                                                                                                                                                                                                                                                                   SEQUENCE OF 744-776 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-91064385; PubMed-2248978;
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                               "Cloning and nucleotide sequence of the isoamylase gene from Pseudomonas amyloderamosa SB-15."; J. Biol. Chem. 263:9271-9275(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amemura A., Chakraborty R., Fujita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-88243808; PubMed-3379068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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            KNOWN AS THE ALPHA-AMYLASE FAMILY. ISOAMYLASE SUBFAMILY
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ipro; 1PR000461;
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                       ANFNTYNTVAQNLIVDSLAYWANTMGVDGFRFDLASVLGNSCLNGAYTASAPNCPNGGYN
                                              SDSAPEHRMFAKLIADSLAVWTTDYKIDGFRFDLMGYHPKAQILSAWERIKALNPDIYFF
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F -> C (IN REF. 1).
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L -> V (IN REF. 1).
GAYT -> AVH (IN REF. 1).
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SGLDLFASPALGGUSYGUGGFPOGWSEWNGLFRDS.
TVWICLRNLGPSAATRTSWVDSRRVVRVEWSVPRQ.
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                                                                                                                                                                                                                                                                                 EMBL; M25247; AAA25855.1; EMBL; A10909; CAA00929.1;
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Hydrolase; Glycosidase: Sima
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HSSP; P10342; 1BF2.
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11-AUG-1992 (Rel. 23, Last sequence up
15-DEC-1998 (Rel. 37, Last annotation
ISOAMYLASE PRECURSOR (EC 3.2.1.68).
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Gen. Microbiol. 135:37-45(1989).
- CATALYTIC ACTIVITY: HYDROLYSIS OF 1,6-ALPHA-D-GLUCOSIDIC LINKAGES IN GLYCOGEN, AMYLOPECTIN AND THEIR BETA-LIMITS [
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    GE PP PR E
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RESULT 8
GLGX_ECOLI

GLIGX_ECOLI STANDARD: PRT; 657 AA. P15067; P76693; O1-APR-1990 (Rel. 14, Created) O1-NOV-1995 (Rel. 32, Last sequence update) 15-JUL-1998 (Rel. 36, Last annotation update) GLYCOGEN OPERON PROTEIN GLGX (EC 3.2.1.-). GLGX OR GLYX.

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Best Local
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                                                                                                                                                                                                                                                                                                  GEGWDSNQSDRFEIASQINLK----GTGIGTFSDRLR---DSVRGGGPFDSG------
                                                                                                                                                                                                                                                                                                                                                                                 KYYMDVVYNHTAEGGTWTSSDPTTAT----IYSWRGLDNTTYYELTSGNQYFYDNTGIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQKDDVIYEVHVRGFTEQDTSIPAQYRGTYYG--AG-----LKASYLASLGVTAVEFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNLTMPHAQKTKAD------
                                                      NWLTYSW-
                                                                                                                                                           --DESGSSNLFQSSGRSPWNSINFIDVHDGMTLKDVYSCNGANNSQAWPYGPSDGGTSTN
                                                                                                                                                                               NVIMDVVYNHTNAAG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----IHESHIRDLSAWDQTVPAELRGKYLALTAGDSNMVQHLKT--LSASGVTHVELL
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                                                                             NRVDYSLQDNNYNVGMPRISDDGSNYEVITRVKEMVATPGEAELKQMTAFYQELTELRKS
                                                                                                        Y SWDQGMSAGTGAAVDQRRAARTGMAF EMLSAGT PLMQGGDEY LRT LQCNNNAY NLDSSA
                                                                                                                                  YKASQEADLAT-----RVRMQAVSLATVMLGQGIAFDQQGSELLRSKSFTRDSYDSGDWF
                                                                                                                                                                                                                                                                        FDAADSNVAIN-RILREFTVRPAAGGSGLDLFAEPWAIGGNSYQLGG-FPQGWSEWNGLF
                                                                                                                                                                                                                                                                                                                             ANFINTYNTVAQNLIVDSLAYWANTMGVDGFRFDLASVLGNSCLNGAYTASAPNCPNGGYN 428
                                                                                                                                                                                                                                                                                                                                                       SDSAPEHRMFAKLIADSLAVWTTDYKIDGFRFDLMGYHPKAQILSAWERIKALNPDIYFF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAGITGAVY-YGYRAWGPNW------PYASNWGKGSQAGFVSDVDANGDRFNPN-- 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYDAQQAN--ITFRVYSSQATRIVLYLYSAGYGVQESATYTLSPAGSGVWAVTVPVSSIK 93
                                                                                                                                                                                                                                             -DALRQNQGIGSGAGVLPNELASLSDDQVRHLADLTRLGMAGNLADFVMIDKDGAAKKGS
656
                           968
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Pred. No. 1.8e
36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A5E4C02EF026A3A4 CRC64
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.8e-11;
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Best Local Sim
Matches 187;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
Blattcher F. R., Plunkett G. IIT, Bloch C.A., Perna N.T., Burland Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F. Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
MBu B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Analysis of the Escherichia coll glycogen gene cluster suggests that catabolic enzymes are encoded among the biosynthetic genes."; Gene 70:363-376(1988).

-!- FUNCTION: THIS PROTEIN.MAY BE PART OF A GLYCOGEN BIOSYNTHETIC/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00128; alpha-amylase; 1.
Clycogen biosynthesis; Hydrolase;
ACT_SITE 336 BY S:
ACT_SITE 443 443 BY S:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; JT0400; BVECGX.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coll.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U18997; AAA58229.1; -. EMBL; AE000419; AAC76456.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P10342; 1BF2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-590 FROM N.A.
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518 KSSEFAGYCDSGSTVEEVLNQLKQSDSQDNPQVQALNTLVAQTDSYNWGYDPFHYTVPEG
                                                                                                     122
                                                                                                                                   406
                                                                                                                                                                                                      353
                                                                                                                                                                                                                                                                    306 GAQLADGGVTFRVWAPTAQQVDVVVYSADKKVIGSHPMTRDSASG-AW-------
                                                                                                                                                                                                                                      13
                                                                                                                                                                     70
                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATABOLIC OPERON BUT IS NOT REQUIRED FOR GLYCOGEN SYNTHESIS. SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY. CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A STOP CODON IN POSITION 507.
                                 KAL--GHPVMINYLKQL---
                                                                 LAUTAGDSNMVQHLKTLSASGVTHVELLPVFDLATVNEFSDKVADTQQPFSRLCEVNSAV 517
                                                                                             NAAIAPKCVVVVDHYDWEDDAPP-----RTPWGSTIIYEAHVKGLTYLHPEIPVEIRGTY
                                                                                                                                  DSALKPD-----GWDNLTMPHAQKTKADLAKMTIHESHIRDLSAWDQTVPAELRGKY 457
                                                                                                                                                                   YGYRVHGPWQ----PAEGHRFNPAKLLIDPCARQIDGEFKDNPLLHAGHNEPDYR-----D
                                                                                                                                                                                                    ----SWQGGSDLKGAFYRYAMTVYHPQSRKVEQYEVTDPYAHSLSTNSEYSQVVDLN 405
                                                                                                                                                                                                                                    GAHYDGQGVNFTLFSAHAERVELCVFDANGQ---EHRYDLPGHSGDTWHGYLPDARPGLR 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EG10381; glgx.; IPR000461; -.
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657 AA;
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73576 MW;
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BY SIMILARITY.
Y -> YY (IN REF
                                                                                                                                                                                                                                                                                                       Score 302.5; DE
Pred. No. 8.1e-1
4; Mismatches 2
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AA9EFC1F67FD0420 CRC64;
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                                                                                                                                                                                                                                                                                                                                        657;
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577
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Query Match
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Matches 166
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Interfro; IPR000461; -.
Pfam; PF00128; alpha-amylase; 1.
Pfam; PF00128; alpha-amylase; Glycosidase.
Glycogen blosynthesis; Hydrolase; Glycosidase.
ACT_SITE 333 333 33 BY SIMILARITY.
ACT_SITE 330 BY SIMILARITY.
ACT_SITE 330 BY SIMILARITY.
ACT_SITE 330 BY SIMILARITY.
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HSSP;
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SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YAMTVY----HPQSRKVEQYEVTDPYAHSLS----TNSEYSQ----VVDLNDSA-LKPDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NMVQHLKTLSASGVTHVELLPV-FDLATVNEFSDKVADIQQPFSRLCEVNSAVKSSEFAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YAFRIHGEFANPQKL-----ILDPYAKAVNGKPDLSSEESRSWFLLSDNRDNAHLAPRA 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VVISEEFDWENDTSPN----TPWAETIVYELHVKGFSQLNEKIPAALRGTYTGL-AHPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----WDNLTMPHAOKTKADLAKMTIHESHIRDLSAWDQTVPAELRGKYLALTAGDS
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                                                                                                                                                                                                                        GMAGNIADFYMIDKDGAAKKGSEIDYNGAPGGYAADPTEVVNYVSKHDNQTLWDMISYKA
                                                                                                                                                                                                                                                                        SYFAEWNDRFRDDLCRFWLWKSGE------IGAFAERFAGSSD
                                                                                                                                                                                                                                                                                                                                                                 LGRDTPDFNSSAQLFTDIKNEPSLQ-NIKLIAEPWD-----IGHYGYQVGNFP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NLA-YLKEL---GVTAVELLPVNFH---INE---
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                                                                                    KHNETNGEENRDGRNENYSYNHGVEGSTESLS----EPQKSAVENNRTFAQSGLLMSLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -NNPLAEFKTMVKAFHK-AGIEVILDVVFNHSAESEQTYPTFSQRGIDDQT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                              -GYHPKAQILSAWERIKALNPDIYFFGEGWDSNQSDRFEIASQINLKGTGIGTF-
                                                                                                                                                                                                                                                                                                                 -SDRLRDSVRGGGPFDSGDALRQNQGIGSGAGVLPNELASLSDDQVRHLADLTRL
                                        -YDSGDWFNRVDYS-----LQDNNYNVGMPRISDDGSNYEVITRVKEMVATPGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.78; ilarity 22.08; Conservative 8
                                                                                                                               ----MQAVSLATVMLGQGIAFDQQGSELLRSKSFTRDS
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Pred. No. 1.2e
81; Mismatches
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                                                                                                                                                                               ----PHTTLNFITAHDGFTLKDLVSYNQ
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.2e-07
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EMBL; L05634; AAA22883.1; -.
EMBL; D31856; BAA06656.1; -.
EMBL; D39985; BAA06260.1; -.
EMBL; D89985; BAA11683.1; -.
EMBL; D89026; BAA11683.1; -.
EMBL; Z99124; CABL5959.1; -.
PIR; S32920; S32920.
Subtilist; BG10797; wapA.
Pfam; PF02018; CBD_6; 1.
Cell wall; Repeat; Signal.
SIGNAL 29 2334
DOMAIN 504 869 3
REPEAT 504 605 1
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Q07833;
Q1-OCT-1994
Q1-OCT-1994
Q1-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yoshida K.-I., Sano H., Seki S., Oda M., Fuji "Cloning and sequencing of a 29 kb region of genome containing the hut and wapa loci."; Microbiology 141:337-343(1995).

-!- FUNCTION: STILL UNKNOWN. NOT INVOLVED IN NOTILITY, SECRETION OR DIFFERENTIATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Molecular analysis of three major wall-associated proteins Bacillus subtilis 168: evidence for processing of the produc gene encoding a 258 kDa precursor two-domain ligand-binding protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
WALL-ASSOCIATED PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1000
                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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Bacteria; Firmicutes;
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                                                                                                                                                                                                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
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STRAIN-168 / 1
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NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-95219088; PubMed-7704263;
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                                                                                                                                                                                                                                                                                                                                                    DOMAIN: HAS TWO LIGAND-BINDING DOMAINS; THE N-TERMINUS, HAS THREE 101 AA REPEATS WHICH ARE RESPONSIBLE FOR CELL WALL BINDING; THE C-TERMINUS CONSISTS OF TWO BLOCKS OF RESIDUES WITH A CONSERVED MOTIF REPEATED 31 TIMES.

SIMILARITY: THE REPEATED MOTIF IN THE C-TERMINUS HAS SOME SIMILARITY TO THE REPEATED IN E.COLI RHS GROUP OF PROTEINS (RHSA-D).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTO THE MEDIUM
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BGSC1A1;
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 OR 32 (POTENTIAL).

WALL-ASSOCIATED PROTEIN.

3 X 101 AA APPROXIMATE TANDEM REPEATS.

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(See http://www.isb-sib.
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n of the Bacillus subtilis
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31 x 21 AA APPROXIMATE TANDEM REPEATS OF X(4)-G-X(4)-[YF]-X-D-X(2)-G-X(4).
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g 5	477 SGVTHVELLPVFDLATVNEESDKVADIQQPFSRLCEVNSAVKSSEFAGY 525 1068 XKVTYSVENDLKKVYDYDGTVTSVDNSGERIVKNOVSANSGEFARVETSV 1118
Qγ	526 CDSGSTVEEVLNQLKQSDSQDNPQVQALNTLVAQTDSYNWGYDPFHYTVPEGSYATDPEG 585
Db	1119 QYSGHRLEKAINAKKETYVYSYDADKKTLLMTOPNG 1154
Qy	586 TTRIKEFRTMIQAIKQDLGMNVIMDVVYNHTNAAGPTDR 624
ф	1155 RKVQYGYNEAGNPTQVIDDAEGLKTTTNTKYEGNNVVEDVDPNDVGTGKATESYQYDKDG 1214
Oy	ESATCCSDS
Db	1215 NYTSYKDAYGTETYEYNKNNDYTKMKDTEGNYTDIAYDGLDAYSETDQSGKSSSAAVYDK 1274
Qy	AKLIADSLAVWTTDYKIDGFRFDLMGYHPKAQILSA
Db	1275 YGNQIQSSKDLSASTNILKDGSFEAQKSGWNLTASKDRRKISVIADKSGVLSGSKALEVL 1334
Qy	PDIYFFGEGWDSNQSDRFEI
DЪ	1335 SQSTSAGTDHGYSSATQTVELEPNTTYTLSGKIKTDLAKSRAYFNIDLRDKDQ 1387
Qy	KKG-SE
Дb	1388 KRIQWIHNEYSALAGKNDWTKRQITFTTPANAGKAVVYMEVDHKDKDGKGKAWFDEV 1444
Qy	TLWDMISYKASQEADLATRVRM
đ	1445 QLEKGEVSSSYNPVQNSSFTSATENWNVSGASVDSEEGFNDDVSLKAARTSASQAGS 1501
Qy	
Ф	1502 VTKQTVVLGQSANDKPVYLTLTGMSKASSVKFTDEKDYSLQANVTYADGS 1551
Q	ELKQMTAFYQELTE
B	1552 TGTYNAKFPSGTQEWNRAAVVIPKTKPINKVDISILFQKSATGTVWFDDIRLIEGSLL 1609
Qy	AVMKRDQQAGLLVMT
Dβ	1610 TKSTYDSNGNYVTKEEDELGYATSTDYDETGKKTSETDAKGEKTTYTYDQADQLTNMTLS 1669
Qy	DGLVVAINAAPESRTLNEFAG
D _D	1670 NGTSILHSYDKEGNEVSKTIRAGADQTYKFEYDVMGKLVKTTDPLGNVLASEYDANSNLT 1729
Qy	AGENSLANGVQIA
дb	1730 KTISPNGNEVSLSYDGT 1746
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G D	OTHETICAL 64.1 KDA PROTEIN RV1562C. 562C OR MTCY48.03.
38	obacterium tuberculosis.
ខ្លួន	nomycetales; Corynebacterineae; Mycobacteriaceae; _TaxID-1773;
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꽃 ??	IN-H37RV; INE-98295987; PubMed-963423
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Hypothetical protein; Hydrolase; Glycosidase.
SEQUENCE 580 AA; 64076 MW; 506190468F44B862 CRC64;
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Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sul
Raylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from complete genome sequence.";
Nature 393:537-544(1998).
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Y T., Jagels
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01-APR-1993 (Rel. 25, Last
01-OCT-1996 (Rel. 34, Last
                                                                                                                           Glycogen
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus caldolyticus.
Bacteria; Firmicutes; Bacillus/Clostridium
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                                                                                                                                                                                                                                                   the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                         DNA
                                                                                                                                                                                                                                                                                                                                                                                                                 Kiel J.A.K.W., Boels J.M., Beldman G., Venema "The glgB gene from the thermophile Bacillus of thermolabile branching enzyme.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE-93208370;
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                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                      FGAHVIRGGGAVGTRFCVWAPHAREV...---RLVGSFNDWNGTNSPLTKVNDEGVW
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01-OCT-1996 (Rel. 34, Lost sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
PROBABLE 1,4-ALPHA-GLUCAN BRANCHING ENZYME (E)
BRANCHING ENZYME).
GLGB OR RV1326C OR MTCY130.11C.
MEDLINE-98295987; PubMed-9634230; Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C. Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C. Gordon S.V., Eiglmeler K., Gas S., Barry C.E. III, Tekaia Badcock K., Basham D., Brown D., Chilingworth T., Connor Davies R., Deviln K., Feltwell T., Gentles S., Hamlin N.,
                                                                                                                                        Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria;
Actinomycetales; Corynebacterineae; My
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01-0CT-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- PATHWAY: THIRD STEP IN GLYCOGEN BIOSYNTHESIS
-1- SUBUNIT: MONOMER (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL
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Glycogen biosynthesis; Transferase; Glycosyltransferase.
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                                                                            QDLGMNVIMDVVYNH----TNAAGPTDRTSVLDKIVPWYYQRLNETTGSVESATCCSDSA
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                             PEHRMFAKLIADSLAVWTTDYKIDGFRFDL.---MGYHPKAQILSAWERIKALNPDIYFFG
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                                                             Q-AGIGVIVDWVPAHFPKDAWALGRFDGTPLYEHSDPKRGEQLDWGTYVFDF-----GR
                                                                                                                                                       QSDSQDNPQVQALNTLVAQTDSYNWGYDPFHYTVPEGSYATDPEGTTRIKEFRTMIQAIK
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Glycogen
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                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
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-I- PATHWAY: THIRD STEP IN GLYCOGEN BIOSYNTHESIS.
-I- SUBUNIT: MONOMER (BY SIMILARITY).
-I- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 269:496-512(1995).
-!- CATALYTIC ACTIVITY: FORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=RD / KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
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Bacteria; Proteobacteria;
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4-ALPHA-GLUCAN BRANCHING ENZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KNOWN AS THE ALPHA-AMYLASE FAMILY
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annotation update)
ENZYME (EC 2.4.1.18) (GLYCOGEN BRANCHING
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STANDARD; PRT; 1861 AA.

AC P38536;

DT 01-OCT-1994 (Rel. 30, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE AMYLOPULLULANASE PRECURSOR (ALPHA-AMYLASE/PULLULANASE) (PULLULANASE DE TYPE II) [INCLUDES: ALPHA-AMYLASE (EC 3.2.1.1) (1.4-ALPHA-D-GLUCAN DE GLUCANOHYDROLASE); PULLULANASE (EC 3.2.1.41) (1.4-ALPHA-D-GLUCAN DE GLUCANOHYDROLASE) (ALPHA-DEXTRIN ENDO-1,6-ALPHA-GLUCCOSIDASE)].

GN AMYB.
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J. Bacteriol. 176:3295-3302(1994).

-I. CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.
-I. CATALYTIC ACTIVITY: STARCH-DEBRANCHING ENZYME, HYDROLYZES (1-6)-ALPHA-GLUCOSIDIC LINKAGES IN PULLULAN AND STARCH TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               thermosulfurogenes).
Bacteria; Firmicutes; Bacillus/Clostridium group;
Thermoanaerobacter group; Thermoanaerobacterium.
<u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matuschek M., Burchhardt G., Sahm K., Bahl H.;
"Pullulanase of Thermoanaerobacterium thermosulfurigenes EM1
(Clostridium thermosulfurogenes): molecular analysis of the gacomposite structure of the enzyme, and a common model for its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. EM1;
STRAIN-OSM 3896 / EM1;
MEDLINE-9425998; PubMed-8195085;
                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                  Multifunctional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
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                                                                                                                                                                                                                                                                                                                                                                             Hydrolase; Glycosidase;
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                                                                                                                                                Local Similarity
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SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.

SIMILARITY: CONTAINS 3 S-LAYER HOMOLOGY (SLH) DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: CELL-BOUND, IT C-TERMINUS MAY SERVE AS S-LAYER ANCHOR.
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SGSDKYGPYWVIPLNKESGCINVIVR-
                         PSNVVVTSGNGKVDLSWLQSDGATGY---NIYRSSVEGGLYEKIASNVTETTFEDANVIN
                                                                                                      RYTRNALVLGSLVLLSGCDNGSSSSSSSSN--PDTPDNQDVVVRLPDVAVPGEAVTAVEN
                                                  QAVIHL-----VDIAGITSSSAADYSSKNLYLWNNE--TCDALSAPVAD--WNDVSTTP 110
                                                                             KFLRDGVTFKDLI-----NNNVSYSISNGQIVIDVPAMSGVML----ISDDGQDLTAPQA 932
                                                                                                                                                                                                                                                                                                                                                                                                                                 PF00395; SLH; 3
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FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
SLH 1.
SLH 2.
SLH 3.
SLH 3.
D -> E (IN AAB00841).
04 MW; 06C23070E453B574
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Pred. No. 0.38;
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BY SIMILARITY.
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06C23070E453B574 CRC64;
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                                                                                                                                                                                                                                                    GNLADFVMIDKDGAAKKGSEIDYNGAPGGYAADPTEV-VNYVSKHDNQTLWDMISYKASQ
 PNDSITR-EEMTAIAMRA
                                                                                                                                                                                                                                  GNV--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WADGLTNSTGQGPNMIAQLGYKYVSGTVYDS-----VYGSVYNSVYGVDDSGFTWVNA 1102
                                                                                                                                                     SSGTITFNATHFSQYAAFEYDKTFNDIKDNWAKDVIEVLASRHIVEGMTDTQYEPNKTVT
                                                                                                                                                                                                                                                                                                        AL----TKDALNQNQ-IQNGVNV-----SIKDNGKPNVTNYVSLSNVVDITISGIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---GWDNLTMPHAQK-TKAD----LAKMTIHE-----SHIRDLSAWDQTVPAELRGKYL
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                                   -YEVITRVKEMVATPGEAELKOMTAFYQELTELRKSS
                                                                             RAEFTAMILRILNIKDETYSGEFSDVKSGDWYANAIEAA----
                                                                                                                     RDSY---
                                                                                                                                                                                                                                                                                                                                                                                   ----GKAKDLIVNSKDKKVVFDITTIGEGQQKVVQISKDILDTSAANGKDIVIKSDNASI 1567
                                                                                                                                                                                                                                                                                                                                                                                                                         MGYHPKAQILSAWERIKALNPDIYFFGEGWDSNQSDRFEIASQINLKGTGIGTFSDRLRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYTVPEGSYATDPEGTTRIKEFRTMIQAIKQDLGMNVIMDVVYNHTNAAGPTDRTSVLDK 630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VNSAVKSSEFAGYCDSGSTVEEVLNQLKQSDSQDNPQVQALNTLVAQTDSYNWGYD--PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A-----LTAGDSNMVQHLKTLSASGVTHVELLPVFDLATVNEFSDKVADIQQPFSRLCE 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VEQYEVTDPYAHSLSTNSEYSQVVDLNDSALKPD--------------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----TSTSGSNSSSTGSGSTGSTSITSNISNTSNTSNTIGVITKNGNVITLTLDA 1511
                                                                                                                                                                                                                                -----TLAKPVEVTLNISK---ANDPRKVAVYYYNPTTNQ--WEYVGGKVDA
                                                                                                                                                                                            ATRVRMQAV----
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                                                                                                               ----DSGDWF-NRVDYSLQDNNYNVGMPRISDDGSN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -GDIGNNDQYKASFTPDKIGQWEYLMRF
YEMLTQYKEEN
                                                                                                                                                                                          ----SLATVMLGOGIAFDOOGSELLRSKSFT
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                                                                             YKAGI -- IEGDGKNAR 1771
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Search completed: April 22, 2001, 09:12:11 Job time: 370 sec

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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1 MLRYTRNALVLGSLVLLSGC......AVLELPQGEAQGAGLPVSSK 1091
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_plant:*
sp_rodent:*
sp_unclassified:*
sp_vertebrate:*
sp_virus:*

SUMMARIES

Result No.	Score 1667.5	Query Match	Query Query Match Length DB 29.6 1798 2 26.7 964 1	10 E	ID Q9KZ11 Q4T386
ωĸ	1503	26.7 25.4	964 962	10	Q41386 081638
4	1424.5	25.3	904	10	048541
5 1	1420	25.2	962	10	095758
6	1405.5	25.0	910	N	Q9RXB0
7	1386.5	24.6	886	10	064454
œ	1326.5	23.5	986	10	P93416
9	722	12.8	668	N	P71095
10	716	12.7	849	N	Q9XDB5
11	692.5	12.3	1938	N	P70983
12	685	12.2	825	N	059319
13	647.5	11.5	718	N	034587
14	630	11.2	718	N	800690
15	605.5	10.7	1072	N	Q9K6N1
16	593.5	10.5	717	N	Q9K7U5
17	367.5	6.5	715	N	Q9KY03
18	362	6.4	715	N	09X947
19	355	6.3	782	N	Q9L1E9

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ALIGNMENTS

Query Match Best Local Similarity 36,4 Matches 397; Conservative	RC STRAIN-A3(2); RA Cerdeno A.M., Parkhill J., Barrell RL Submitted (MAY-2000) to the EMBL/GI RN [3] RP SEQUENCE FROM N.A. RC STRAIN-A3(2); RA Redenbach M., Kieser H.M., Denapal' RA Kinashi H., Hopwood D.A.; RA Kinashi H., Hopwood D.A.; RT the 8 Mb Streptomyces coelicolor A. RL Mol. Microbiol. 21:77-96(1996). DR EMBL; AL355752; CAB90874.1; SQ SEQUENCE 1798 AA; 194106 MW; 4:		SUL KZ1
5%; Score 1667.5; DB 2; Length 1798; 8%; Pred. No. 4.4e-97; 166; Mismatches 391; Indels 137; Gaps	STRAIN-A3(2); Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.; Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases. [3] SEQUENCE FROM N.A. STRAIN-A3(2); Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Redenbach H., Hopwood D.A.; Redenbach H., Hopwood D.A.; "A set of ordered cosmids and a detailed genetic and physical map for "A set of ordered cosmids and a detailed genetic and physical map for "A set of ordered cosmids and a detailed genetic and physical map for "A set of ordered cosmids and a detailed genetic and physical map for "Ast optional complex coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996). EMBL; AL355752; CAB90874.1; ". EMBL; AL355752; CAB90874.1; ".	Streptomyces coelicolor. Streptomyces coelicolor. Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Bacteria; Firmicutes; Streptomycineae; Streptomycetaceae; Streptomyces. NCBL_TaxID=1902; [1] [1] [2] [3] Segor K.J., Harris D.; Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases. SEQUENCE FROM N.A.	T 1 OPECIAL PRELIMINARY; PRT; 1798 AA. OPKZ11; PRELIMINARY; PRT; 1798 AA. OPKZ11; PRELIMINARY; PRT; 1798 AA. OL-OCT-2000 (TrEMBLrel. 15, Created) O1-OCT-2000 (TrEMBLrel. 15, Last annotation update) O1-OCT-2000 (TrEMBLrel. 15, Last annotation update) O1-OCT-2000 (TREMBLRel. 15, Last annotation update) O1-OCT-2000 (TREMBLRel. 15, Last annotation update)
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GLRVVMDVVYNHTAASGQA-KTSVLDRIVPGYYQRL-LADGSVANSTCCSNTATENAMMG
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                            TLPAWSVAVLE
                                                                                                                CPQITGASAAYRDLLRIRSGEQDFSLATAARVQSRLSFPLSGEDETPGVITM----
                                                                                                                                                                                         ELLRSKSFTRDSYDSGDWFNRVDYSLQD-NNYNVGMPRISDDGSNYEVITRVKEMVATPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LADGGVTFRVWAPTAQQVDVVVYSADKKVIGSHPMTRDSASGAWSWQGGSDLKGAFYRYA 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TLLWPGGQDKPIVRLYYSHSSKVAADGEGKFT---DRYLKLTPTTVSQQVSMRFPHLSSY
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                                                         -----RLGDLVVVFNATPERQEQRVGAAAGTGYRLHPVQAAGADAVVKESAYAAKTGTF
                                                                                  GASLDSRLDGLVVAINAAPE--SRTLNEFAGETLQLSAIQQTAGENSLANGVQIAADGTV 1064
                                                                                                                                          EAELKQMTAFYQELTELRKSSPLFTLGDGSAVMKRVDFRNTGSDQQAGLLVMTVDDGMKA 1006
                                                                                                                                                                        DLLRSKSLDRNSYDSGDWFNALHWNCADGNGFGRGLPPAADNQDKWPYAKPLLGAVEV-G
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Q41386;
ID Q41386;
AC Q41386;
AC Q41386;
DT 01-NOV-1996;
DT 01-NOV-1996;
DT 01-NOV-1996;
OF PULLULANASE.
GN PULSPO.
OS Spinacia ole:
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OX NCBI_TAXID=3;
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OX NCBI_TAXID=3;
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TAXID=3;
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Best Local Similarity 36.2
Matches 365; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spinacia oleracea (Spinach).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; endicotyledona; core eudicots; Caryophyllidae;
Caryophyllales; Chenopodiaceae; Spinacia.
NCBI_TaxID=3562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Renz A., Schmid R., Kossmann J., Beck E.;
Submitted (JAN-1995) to the EMBL/GenBank/DDBJ
EMBL, X83969; CAS580031; -.
MENDEL; 16403; Spiol;2480;16403.
INTERPRO; IPR000461; -.
PFAM; PF00128; alpha-amylase; 1.
CHAIN 65 964
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::||:||:||:||:||
TLLADLSSETLKPEGWENLADEKPHLLSP----SDISLYELHIRDFSAYDLTVHPDLRGG 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALAEAHWYDKNTLLW----PGGQDKPIVRLYYSHSSKVAADGEGKFTDR-------YLKL 231
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                                                          LR-RUNDGALENSTCVNDTASEHFMVERLILDDLKHWAVNYKVDGFRFDLMGHIMKHTMV
                                                                                    QRLNETTGSVESATCCSDSAPEHRMFAKLTADSLAVWTTDYKIDGFRFDLMGYHPKAQIL
                                                                                                                                                                                                  GSYATDPEGTTRIKEFRTMIQAIKQDLGMNVIMDVVYNHTNAAGPTDRTSVLDKIVPWYY
                                                                                                                                                                                                                                                                                                                                                                                                                          YLALTAGDSNMVQHLKTLSASGYTHVELLPVFDLATVNEFSDKVADIQQPFSRLCEVNSA
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                                                                                                                                                                     GSYATDPNGPCRIIEFRKMVQALNR-IGLRVVLDVVYNHLNSSGPSDDNSVLDKIVPGYY
                                                                                                                                                                                                                                                                                 -KKWKF-----VDTKRFETLPPDSEEQQAQITAIRDEDGYNWGYNPVLWGTPK
                                                                                                                                                                                                                                                                                                                 VKSSEFAGYCDSGSTVEEVLNQLKQSDSQDNPQVQALNTLVAQTDSYNWGYDPFHYTVPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26.7%; Score 1503; DB 10; 36.2%; Pred. No. 4.5e-87; tive 169; Mismatches 324;
- IYFFGEGWDSNQ - -
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  -SDRFEIASQINLKGTGIGTFSDRLR
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Best Local S
Matches 336
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Submitted (JUL-1998) to the EMBL/GenBank/DDBJ
EMBL; AF080567; AAD11599.1; -
MENDEL; 32273; Zeama; 2480; 32273.
SEQUENCE 962 AA; 106239 MW; 5F5AAB7C6EBD5D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1998 (TIEMBLIEL 08, Created)
01-NOV-1998 (TIEMBLIEL 08, Last sequence update)
01-NOV-1999 (TIEMBLIEL 12, Last annotation update)
PULLULANASE-TYPE STARCH DEBRANCHING ENZYME.
                                                                                                                                                                                                                                                                                                                                     Beatty M.K., Rahman A., Myers A.M., James M.G.; "Genetic and biochemical characterization of ZPUI, a pullulanase-type
                                                                                                                                                                                                                                                                                                                                                                                                        Zea mays (Maize).
Eukaryota; Viridiplantae;
Magnoliophyta; Liliopsida;
NCBI_TaxID=4577;
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                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                     GVALAE-----AHWVDKNTLLWPGGQDKPIVRLYYSHSSKVAADGEG-KFTDRYL
                                                                                                                                                    GVAVAESAQGFLLDARAYWVTKSLIAWNISDQKTSLFLYASRNATHCMSSQDMKGYDSKV
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                                                                                                   ELQPENDGLPSSVTQKFPFISSYRAFRIPSSVDVATLVKCQLAVASFDAHGNRQDVTGLQ
                                                                                                                            KLTPTT--VSQQVSMRFPHLSSYAAFKLPDNANVDELLQGETVAIAAAEDGILISATQVQ
                                                                                                                                                                                                           336;
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                        -- DSASGAWSWQGGSDLKGAFYRYAMTVYHPQSRKVEQYEVTDPYAHSLSTNSEYSQVVD
                                                                                                                                                                                                                                                                                                                                                                              FROM N.A.
                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                      25.48;
                                                                                                                                                                                                           173;
                                                                                                                                                                                                                                                                                                                                                                                                                      Embryophyta; Tracheophyta; poales; Poaceae; Zea.
                                                                                                                                                                                                         Score 1432.5; DB
Pred. No. 1.4e-82;
73; Mismatches 338
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O1-JUN-1998 (TrEMBLrel. C
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LOK F., Kristensen M., Planchot V., Leah R., S
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ
EMBL; AF022725; AAD04189.1;
MENDEL; 27102; Horvu; 2480; 27102.
INTERPRO; IPR000461;
PFAM; PF00128; alpha-amylase; 1.
                                                                                                                                                                                                                                                                            1039
                                                                                                           Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; !
Magnoliophyta; Liliopsida;
  SEQUENCE
                                                                                                  NCBI_TaxID=4513;
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                                                                                                            Embryophyta; Tracheophyta; Poales; Poaceae; Hordeum.
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Last sequence update)
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                                                                                                                                                        GVQIAADGTVTLPAWSVAVLELPQ
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                                                                                                                  SAYEAATGRETVPGRTVSVFVEPR
                                                                                                                                                                                                                                        VDDGMKAG---ASLDSRLDGLVVAINAAPE--SRTLNEFAGETLQLSAIQQTAGENSLAN
                                                                                                                                                                                                                                                                                                NPSFKPAKGHILAALDSFVDILKIRYSSPLFRLSTANDIKQRVRFHNTGPSLVPGVIVMG
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MEDILINE-99169277; PubMed-10069825;
Burton R.A., Zhang X.Q., Hrmova M., Fincher G.B.;

"A single limit dextrinase gene is expressed both endosperm and in germinated grains of barley.";
Plant Physiol. 119:859-872(1999).

EMBL; AF122050; AAD34348.1; -.

EMBL; AF122049; AAD34347.1; -.
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Eukaryota; Viridiplantae; 1
Magnoliophyta; Liliopsida;
NCBI_TaxID=4513;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation updat
LIMIT DEXTRINASE.
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IQIGLAGNLRDYVLISHTGEAKKGSEIHTFDGLPVGYTASPIETINYVSAHDNETLFDVI
                                                                               GIGSFNDRIRDAINGGNPF--GNPLQ--QGFNTGLFLEPNGFYQGNEADTRRSLATYADQ
                                                                                                                                                                                                       MGYHPKAQILSAWERIKALNPD-----IYFFGEGWDSNQ---SDRFEIASQINLKGT
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                                          TRLGMAGNLADFVMIDKDGAAKKGSEI-DYNGAPGGYAADPTEVVNYVSKHDNQTLWDMI
                                                                                                                                                                             MGHIMKRIMMRAKSALQSLTTDAHGVDGSKIYLYGEGWDFAEVARNQRGINGSQLNMSGT
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01-JUN-2000 (Tr
ALPHA-DEXTRAN E
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                                                                                                                                                                                                                                                                                                                                                                           radiodurans R1.";
Science 286:1571-1577(1999).
EMBL; AE001900; AAF09983.1;
TIGR; DR0405; -
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L-JUN-2000 (TrEMBLrel. 14, Last annotation updat
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                                                                                    AEAAEALSYGAQLADGGVTFRVWAPTAQQVDVVVYSADKKV1GSHPMTRDSASGAWSWQG
                                                                                                                                  AIMLSRDLIVVKPALAQPGAW----LTLHVSPTATLKLGADGVSGGDTLALEEVEGGLTP
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DQSWKGLAYRFEVRVFAPSTGNIETNLVTDPYSVALTRNSTHSVFADLSDNSQKPAGWNA
                            GSDLKGAFYRYAMTVYHPQSRKVEQYEVTDPYAHSLSTNSEYSQVVDLNDSALKPDGWDN
                                                                                                                ALQAKAPYLAGYKLLQIRAADRAKLPTALSGQLAVSSYLPGGKVLDATGVQTAWALDDLY
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larity 35.3%;
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Pred. No. 6.4e
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01-AUG-1998 (TrEMBLrel.
01-AUG-1998 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
                                                                                                                                            Oryza sativa (Rice).
Eukaryota; Viridiplantae; Embryophyta; Trach
Magnoliophyta; Liliopsida; Poales; Poaceae;
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                      Submitted (APR-1998) to the EMBL/GenBank/DDBJ EMBL; AB012915; BAA28632.1; MENDEL; 28470; Oryse; 24480; 28470.
INTERPRO; IPR000461;
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Francisco P.B., Zhang
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            PFAM; PF00128;
                                                                          Nakamura Y.
                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                   NCBI_TaxID-4530;
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                                                                                                                                                                                                                                                                                                               ----ASVPALTTAV
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                                                                                                                                                                                                                                                 PRELIMINARY;
alpha-amylase;
AA; 109858 MW;
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                                                                                    Y., Park
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13,
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 9D537693EF154A4E CRC64;
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ceae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     HFASVDDNKSNWKFVD------EAQLAKLPPGSDEQ
                                                                                                                                                                                                                                                                      DPTEVVNYVSKHDNQTLWDMISYKASQEADLATRVRNQAVSLATVMLGQGTAFDQQGSEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NVIMDVVYNHTNAAGPTDRTSVLDKIVPWYYQRLNETTGSVESATCCSDSAPEHRMFAKL
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KGRFTVPRRTTAVFVQPR 987
                             DGTVTLPAWSVAVLELPQ 1078
                                                            EKCKMAQLDKNFSYVVTIFNVCPHEVSIEIHDLASLGLELHPIQVNSSDALVRQSAYEAS
                                                                                        AG---ASLDSRLDGLVVAINAAPE--SRTLNEFAGETLQLSAIQQTAGENSLANGVQIAA 1060
                                                                                                                       LKNHILSAFDNEVDILKIRYSSPLERLSTASDIEQRVREHNTGPSMVPGVIVMSIKDAQN
                                                                                                                                            LKQ--MTAF--YQELTELRKSSPLFTLGDGSAVMKRVDERNTGSDQQAGLLVMTVDDGMK 1005
                                                                                                                                                                                                     LRSKSFTRDSYDSGDWFNRVDYSLQDNNYNVGMPRISDDGSNYEVITRVKEMVATPGEAE
                                                                                                                                                                                                                                                   SPVETINYVSAHDNETLFDIVSIKTPIGLSIDEKCRINHLASSMIALSQGIPFFHAGDEI
                                                                                                                                                                                                                                                                                                             FGEVAQNKRGINASQINMSGTGIGSFNDRIRDSVNGGNPF--GNPLQ--QGFSTGLFLEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GPLLQTVQLKELNGVWSVTVPRYPENQYYLYEVKVYHPSTSQVEKCLADDPYARGLSANG
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                                                                                                                                                                                      LRSKSLDRDSYNSGDWFNKLDFTYETNNWGVGLPPRDKNEENWHLI----KPRLENPSFRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----QAAIVSIQQEDPYNWGYDPVLWGVPKGSYASNPDGPSRIIEYRQMVQALNR-IGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative 164; Mismatches 359; Indels 117; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24.6%; Score 1386.5; DB 10; 34.6%; Pred. No. 1.2e-79;
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SIGNAL
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193416;
01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
STARCH DEBRANCHING ENZYME PRECURSOR.

Oryza sativa (Rice).

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza.

MCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-CV. FUJIHIKARI; TISSUE-ENDOSPERM;

MEDLINB-96275956; PubMed-8680309;

Nakamura Y., Umemoto T., Ogata N., Kuboki Y., Yano M., Sasaki T.;

"Starch debranching enzyme (R-enzyme or pullulanase) from developing rice endosperm; purification, cDNA and chromosomal localization of the gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Planta 199:209-218(1996).
EMBL; D50602; BAA09167.1; -. 0.
MENDEL; 16402; Orysa;2480;16402.
INTERPRO; IPR000461; -.
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|:| |: | | | | | | | | |
                                                                                                                                                                                                                  HPMTR----DSASGAWSWQGGSDLKGAFYRYAMTVYHPQSRKVEQYEVTDPYAHSLSTNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GRDGVGEECAAAVASQGFVTDARAYWVTRSLIAWNVNDQDTSLFLYASRDATMHVSDGAI 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GNSAVYDSRADAFRAAFGVALAEAHWVDKNTLLWPGGODKPIVRLYYSHSSKV-AADGEG
                                                NVIMDVVYNHTNAAGPTDRTSVLDKIVPWYYQRLNETTGSVESATCCSDSAPEHRMFAKL 665
                                                                                           ----QAAIVSIQQEDPYNWGYDPVLWGVPKGSYASNPDGPSRIIEYRQMVQALNR-IGL
                                                                                                           DNPQVQALNTLVAQTDSYNWGYDPFHYTVPEGSYATDPEGTTRIKEFRTMIQAIKQDLGM
                                                                                                                                                                                                                                                                                                  EYSQVVDLNDSALKPDGWDNLTMPHAQKTKADLAKMTIHESHIRDLSAWDQTVPAELRGK 456
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                                                                                                                                                       HFASVDDNKSNWKFVD---------EAQLAKLPPGSDEQ
                                                                                                                                                                                                                                                 YLAL-----TAGDSNMVQHLKTLSASGVTHVELLPVF
IADSLAVWTTDYKIDGFRFDLMGYHPKAQILSAWERIKALNPD--
                             RVVMDVVYNHLDSSGPFGVSSVLDKIVPGYYLRRN-VNGQIENSAAMNNTASEHFMVDRL
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109592 MW; FBAB89E1634CAD27 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      D'Elia J.N., Salyers A.A.;

"Contribution of a neopullulanase, a puglucosidase to growth of Bacteroides the J. Bacteriol. 178:7173-7179(1996).

EMBL; U67061; AAC44685.1;

INTERPRO; IPRO00461;

PFAM; PF00128; alpha-amylase; 1.

SEQUENCE 668 AA; 74603 MW; 044D3D6.
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01-FEB-1997 (
01-FEB-1997 (
01-MAY-2000 (
PULLULANASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; CFB 9
NCBI_TaxID-818;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteroides thetaiotaomicron.
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les 215; Conserv
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                                                                                                                                                                                                                                                                    VQTAGVLDDAYAEAAEALSYGAQLADGGVTFRVWAPTAQQVDVVVYSADKKVIGSHP---
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AAIIDWQST--NPDGWESDTRP-PLKSPAD---MIIYEMHHRDFSV-DSTSGVKNKGKYL
                                                                                                                                                                                                                    VRTGSLIEMEYTPEA - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IKDAQNEKCKMAQLDKNFSYVVTIFNVCPHEVSIEIHDLASLGLELHPIQVNSSDALVRQ
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                                                                                                        VKMQSGEEGTWTAVVSKDLIGKFYTFNV-----KIDDKWQGDTPGINARAVGVNGKR
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                                                                                                                                                              -MTRDSASGAWSWQGGSDLKGAFYRYAMTVYHPQSRKVE---QYEVTDPYAHSLSTNSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 02, Created)
(TrEMBLrel. 02, Last sequence update)
(TrEMBLrel. 13, Last annotation update)
                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                         %; Score 722; DB 2;
%; Pred. No. 1.1e-37;
117; Mismatches 231
                                                                                                                                                                                                                                                                                                                                                                                                                                     1.
044D3D62578C6845 CRC64;
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                                                                                                                                                                                                                    -TKFTLWSPTADEVRLMLYEAGE---GGHAYET
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C STRAIN-DSM 9078;

X MEDLINE-99240435; PubMed-10224005;

A Bertoldo C., Duffner F., Jorgensen P.L., Antranikian G.;

A Bertoldo C., Duffner F., Jorgensen P.L., Antranikian G.;

Fullulanase type I from fervidobacterium pennavorans ven5

I sequencing, and expression of the gene and biochemical

T characterization of the recombinant enzyme.";

Appl. Environ. Microbiol. 65:2084-2091(1999).

BR EMBL; AF096862; AAD30387.1; -.

PROSITE; PS00626; RCC1_2; UNKNOWN_1.

SEQUENCE 849 AA; 96591 MW; 1CB6B2A882A351A2 CRC64;
                                                                                                                                                                                                                                                                           Q9XDB5;
Q9XDB5;
Q1-NOV-1999
Q1-NOV-1999
Q1-MAY-2000
                                                                                                                                                                                                                                                             PULLULANASE
                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                      Bacteria;
                                                                                                                                                                                                                                  Fervidobacterium pennivorans
                                                                                                                                                                                                    NCBI_TaxID=93466;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OVOCD-----SVNYTOKP--WAKQPVQMISYVSCHDGLCLVDRL--KASM-PDITPEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIDKDGAAKKGSEIDYNGAPGGYAADPTEVVNYVSKHDNQTLWDMISYKASQEADLATR- 863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PKAQILSAWERIKALNPDIYEFGEGWDSNQSDRFEIASQINLKGT-----GIGTFSDRLR 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALTA-GDSNM------VQHLKTLSASGVTHVELLPVFDLATVNEFSDKVADIQQPFSRLC 511
                                                                                                                                                                                                                                                                                                                                                                                                           EFLPV---EGSNLIAFRLKDHANG-----DHWEDIIVAFNSRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DGLCGPVGDKRKGAFL-----
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                                                                                                                                                                                                                 Thermotogales;
                                                                                                                                                                                                                                                             (TrEMBLrel.)
(TrEMBLrel.)
(TrEMBLrel.)
                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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13,
                                                                                                                                                                                                                   Fervidobacterium
                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation updat
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Query Match Best Local Similarity

12.78;

Matches

243;

Conservative

139;

Score 716; DB 2; Pred. No. 4.1e-37; 39; Mismatches 315

Length 849;

Indels

286;

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                                                                                                                                                                                                                WTTDYKIDGFRFDLMGYHPKAQILSAWERIKALNPDIYFFGEGWDS-NQSDRFEIASQIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --EYRESVDYFSKAVTKNSAKSAIIDF--SKINPESWEXVARPPLVAPEDAI----IYEI
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                                                                                  ELRKSHIAFRORTAEDIRKKLTF
                                                                                                              ELRKSSPLFTLGDGSAVMKRVDF
                                                                                                                                          SPISINGLDYA----
                                                                                                                                                                                              *NYLAAQ*AD*-TTVKWTEEMLKDAQKLAGAILLTSQGIPFLHAGQDFARTKKFDENSYK 722
                                                                                                                                                                                                                                                                                                              VGGTGIAAFNDEFRDALRG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YSH-----SSKVAADGEGKFTDRYLKLTPTTVSQQVSMRFPHLSSYAA--FKLPD-NA 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ITIKDGKAEVWLLQGIEQIYTTKPDT------SPRVLFAQARDQYTIEAY
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                                                                                                                                                                   SGDWFNRVDYSLQDNNYNVGMPRISDDGSNYEVITRVKEMVATPGEAELKQMTAFYQELT
                                                                                                                                                                                                                                                     ----LMGALA-----KETGVKRGVAGSIEYDEVIRSFAKDPQETINYVEVHDNHTLWDK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AVTAVENQAVIHLVDIAGITSSSAADYSSKNLYLWNNETCDALSAPVADWNDVSTTPSGS
              PRELIMINARY;
                                                                                                              984
              PRT;
              1938
                                                                                                                                          -----RKAEFIDVFNYYKGLI
              AA
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Best Local Similarity
Matches 281; Conserv
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Hatada Y., Igarashi K., Ozaki K., Ara K., Hitomi J., Kobayashi T.,
Kawai S., Watabe T., Ito S.;
"Amino acid sequence and molecular structure of an alkaline
amylopullulanase from Bacillus that hydrolyzes alpha-1,4 and alpha-1,6
linkages in polysaccharides at different active sites.";
J. Biol. Chem. 271:24075-24083(1996).
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01-FEB-1997 (TrEMBLrel. 02, Last seq
01-OCT-2000 (TrEMBLrel. 12, Last ann
ALKALINE AMYLOPULLULANASE.
Bacillus sp.
1340
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PFAM; PF00746; Gram_pos_anchor; 1.
PROSTTE; PS00133; CARBOXYPEPT_ZN_2; UNKNOWN_1.
SEQUENCE 1938 AA; 214917 MW; A29D3F715EB6A72E
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INTERPRO: IPRO00834; -.
INTERPRO: IPRO01899; -.
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                                                                                                                                                                                                                                                                                                                                                                                                 -RGVWSVKLTKDNTGLDSLKGYYYHYEIT------HGDVTNLALDPYAKSMAAWNN 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIDEMYAYDGK---LGAELHEDGTATLKVWSPKADNVSVVLYDKVDQNEVVDTIEMVKGD 1190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEELKEQLEIKDVDGNDVSFTDVTIEGEKTVHVHGEFDLEKIPFSVTYLDRTISVKSGWK 1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----ERTNADYEGWGLWNWED-----VESPSDGWPNGAADAAGIGKYGAYYDIKLKEDA 1000
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                                                           CEVNSAVKSSEFAGYCDSGSTVEEVLNQLKQSDSQDNPQVQALNTLVAQTDSYNWGYDPF 570
                                                                                                                                                                                         AELRGKYLALTAGDSNMVQHLKTLSASGVTHVELLPVFDLATVNEFSDKVADIQQPFSRL 510
                                                                                                                                                                                                                                                                EAGDKVGKAAIVDI--GSIGPE-LDYADIPGFEKREDTI----IYEVHVRDFTS-DPNIG
                                                                                                                                                                                                                                                                                                                                  E----YSQVVDLNDSALKPDGWDNLTMPHAQKTKADLAKMTIHESHIRDLSAWDQTVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASGAWSWQ-----GGSDLKGAFYRYAMTVYHPQSRKVEQYEVT----DPYAHSLST-NS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -- QYNQLEVKEGEDKYYTNPYGTYPLALYSGEVLSD------KLISLTFTRTEGLD 1073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WVDKNTLLWPGGQDKPIVRLYYS-----HSSKVAADGEGKFTDRYLKLTPTTVSQQVSMR 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NKIGFLEVN------KQSGGQTGDMTFDMLK------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IGFLVLNTTNGDKDGGDKAVELFSPDL--NEIWIKQGSDEVFLYEPVDLPANTVRIHY--
FE----
                                                                                                                              EDLKAQFGTF - - - - ASFVEKLDYIQELGVTHIQLLPVMSYYFSNEF - - - - - ESGERM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FPHLSSYAAFKLPDNANV---DELLQGETVAIAAAE---DGILISATQV-QTAGV----
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24.2%; Pred. No. 5.1e-35;
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Q59319;
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01-NOV-1996 (Tremblrel. 01, Last sequence update)
01-MAY-2000 (Tremblrel. 13, Last annotation update)
ALPHA-DEXTRIN 6-GLUCANOHYDROLASE (EC 3.2.1.41)
(ALPHA-DEXTRIN ENDO-1,6-ALPHA-GLUCOSIDASE) (PULLULANASE)
(PULLULAN 6-GLUCANOHYDROLASE) (LIMIT DEXTRINASE) (DEBRANCHING
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INTERPRO; IPRO00461; -
PFAM; PF00128; Alpha-amylase;
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                                                                                                                                                          Hydrolase;
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. J. Blochem. 0:0-0(0).
CATALYTIC ACTIVITY: STARCH-DEBRANCHING
ALPHA-GLUCOSIDIC LINKAGES IN PULLULAN A
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825 AA; 95
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Lapidus A.,
Submitted (JI
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               SEQUENCE FROM N.A.
Lapidus A., Galleron
Submitted (JUN-1997)
                                                                 Bacteria; Firmicutes; Bacillus/Staphylococcus NCBI_TaxID-1423;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DSALKPDGW-----DNLTMPHAQKTKADLAKMTIHESHIRDLSAWDQT--VPAELRGKY 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AENGTWDVYLPGDLKNHFYLYEIWHYNYEDDEGYIVYHVPDPYSKASSSNSGKSYIFDPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DSVRGGGPFDSGDALRQNQGIGSGAGVLPNELASLSDDQVRHLADLTRLGMAGNLADFVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YQCPEYWYSTKSGGIEALKELRTMIKKLHEN-GIGVVMDVVFNHTYHTKG--GKFSIFDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YTVPEGSYATDPEGTTRIKEFRTMIQAIKQDLGMNVIMDVVYNHT-NAAGPTDRTSVLDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGFCQEGYYKEGISTGLLHLKEL - - - GVTHVHLLPISDFGSVDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DGLI--DGWQADSFVDNI-----EKQDDA--IIYEMHVRDFTI-DQSSGIGENLRGKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SASGAWSWOGGSDLKGAFYRYAMTVY-HPQSRKVEQYEVTDPYAHSLSTNSEYSQVVDLN 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YARPREILTRNEYFYAGELGARYEPYGTYFRLWAPTAYKVKIQIFDEHENFKFGKEMSR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       217;
                                                                                                                                                                                                                                                                                                                                                                                                                  -GRLKQG----IKAAIDDFAKEPDECVNYVSCHDNLTLFDKLQKTMVGEDIFWIDRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----DLDGYKTGY----
                                                                                                                                                                                                                                                                                                                                                                  -LANAIVLTSQGVAFLHGGVEFNRSKGGHPNTYNAGDNINKIDWSLKEKFFDT •
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                                                                                                                                                                                                 PRELIMINARY;
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                  6
                                                                               Bacillus/Clostridium us group; Bacillus.
                  the
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                                                                              group;
              Sorokin A., Ehrlich I
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                                                                                                                                             Last sequence update)
Last annotation updat
                                                                                                                                                                       Created)
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                              Ehrlich D.
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                                                                                          group;
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                                                                                                                                             update)
                 databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Borriss R., Bourster L., Brans A., Braun M., Brignell S.C., Bron S., Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T., Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D., Erit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kunst F., Ogasawara N., Yoshikawa H., Danchin Submitted (NOV-1997) to the EMBL/GenBank/DDBJ EMBL; AF008220; AAC00283.1; -
EMBL; Z99119; CAB14971.1; -
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  294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
les 224; Conserv
PLHFFAPEGSYASNPHDPQTRKTELKQMINTLHQH-GLRVILDVVFNHVYKR----ENSP
                                            PFHYTVPEGSYATDP-EGTTRIKEFRTMIQAIKQDLGMNVIMDVVYNHTNAAGPTDRTSV
                                                                                                                                                                                                                   KYLALTA-----GDSNMVQHLKTLSASGVTHVELLPVFDLATVNEFSDKVADIQQPFS
                                                                                                                                                                                                                                                                                                                                                                                 GRTFQMTR-LEKGYYAVTVTGDLHG--YEYLFCI----CNNSEWMETVDQYAKAVTVNGE 190
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                                                                                                                                    RLCEVNSAVKSSEFAGYCDSGSTVEEVLNQLKQSDSQDNPQVQALNTLVAQTDSYNWGYD
                                                                                                                                                                                        KYLALTETDTQTANGSSSGLAYVKEL---GVTHVELLPVNDFAGVDE-----EKPL-
                                                                                                                                                                                                                                                                                      KGVV-----LRPDQMKWTAPLKPFSHPVDA----VIYETHLRDFSIHENSGMIN-KG
                                                                                                                                                                                                                                                                                                                                  YSQVVDLNDSALKPD--GWDNLTMPHAQKTKADLAKMTIHESHIRDLSAWDQTVPAELRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IRTAAFDDEFYYDG----ELGAVYTADHTVFKVWAPAATSAAVKL-----SHPNKS
                                                                                                                                                                                                                                                                                                                                                                                                                             MTRDSASGAWSWQGGSDLKGAFYRYAMTVYHPQSRKVEQYEVTDPYAHSLSTNSE 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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aa; 81104 MW;
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96f9EB7667B77E93 CRC64;
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databases
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                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                       Matches 232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        069008;
069008;
01-AUG-1998
01-AUG-1998
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kim T.J., Kim J.W., Park K.H.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ
EMBL; AF060205; AAC15073.1; -
INTERPRO; IPR000461; -
PFAM; PF00118; alpha-amylase; 1.
SEQUENCE 718 AA; 80446 MW; 8F7C0D22405EA8A
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Hacteria; Thermus/Deinococcus
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                                                          270 VAIAAAEDGILISATQVQTAGVL-----DDAYAEAAEALSYGAQLADGGVTFRVWAPTAQ 324
                                                                                                                                                                                                                                                                                                      150 AFGDFTDRTVSVIAGNSAVYDSRADAFRAAFGVALAEAHWVDKNTLLWPGGQDKPIVRLY 209
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74 YWVRSCRG----EETDVQIGAVVRTPAFDDRFFYDG----PLGAEYLKEQTVFRVWAPTAT 126
                                                                                                                               48
                                                                                                                                                                                YSHSSKVAADGEGKFTDRYLKLTPTTVSQQVSMRFPHLSSYAAFKLPDNANVDELLQGET 269
                                                                                                                                                                                                                                              AYLDEMDQIV-VLAPKSLGFDGMAPF------TLVAPSGEEIP---LS 47
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                                                                                                                               VQHVEDV---GE---TVKYV-----
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  Query Match
Best Local Similarity
                                                                         SEQUENCE FROM N.A.

STRAIN-C-125 / JCM 9153;

Takami H., Nakasone K., Takaki Y.;

Takami H., Nakasone K., Takaki Y.;

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AP001519; BAB07416.1; -.

SEQUENCE 1072 AA; 120674 MW; 5264235CF24619D9 CRC64;
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                                                                                                                                                                                                                   Bacillus/Staphylococcus NCBI_TaxID-86665;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---VDIAGITSSSAADYSSKNLYLWNNETCDALSAPVADWNDVSTTPSGSD------K 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAENIGFLVL-----NTATGDKDGND-KHVQLLSPEM----KEIWIKEGSDDVFL 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NALVIGSIVILISGCDNGSSSSSSSSSSPDTPDNQDVVVRLPDVAVPGEAVTAVENQAVIHL 66
                                                                                                                                                                                                                                                                                                                                             LADLTRLGMAGNLADFYMIDKDGAAKKGSEI--DYNGAPGGY-AADPTEVVNYVSKHDNQ 844
                                                                                                                                                                                                                                                                                                                                                                                                                      QDWMQHTESVGVFSDEFRNELK-----SGFG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YNHTAA-----VEIFEDLMPNYYHEW-DADGTPRTSFGGGRLGTTHKMSRRILVDSITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YNHTNAAGPTDRTSVLDKIVPWYYQRLNETTGSVESATCCSDSAPEHRMFAKLIADSLAV 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NEFSDKVADIQQPFSRLCEVNSAVKSSEFAGYCDSGSTVEEVLNQLKQSDSQDNPQVQAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FADKTYVARAGWRLIDALYGYDGE----LGAVLHEDGSSTLTFWSPLADHVSVVLYDKDDQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIWLSEDDLAEQIHLTDTNGASVAFDHVT-----IHDEKTV--ILHGSFDAELAPYHVT 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T-----TVSQQVSMRFPHLSSYAAFKLPDNANVDEULQGETVAIAAAEDGI 279
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  YPIHHLTR ---
                                                                                                      GGQAPYKSTYMTDENGKPFVYPYFIHDSYDSSDAINKFDWGKATNK------EK 898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WTTDYKIDGFRFDLMGYHPKAQILSAWERIKALNPDIYFFGEGWDSNQSDR----FEIAS 728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---VIGSHPMTRDSASGAWSW------QGGSDLKGAFYRYAMTVYHPQSRKVEQYEVT-- 385
                                                                                                                                                                                                             TLHDVIAQSIRKDPEYHQEEIHKRIRL---GNTMVLTAQGTAFLHAGQEFGRTKQFRADT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NNYNWGYDPHSYFSLSGMYSENPEDPELRIKEFKHLIDEIHR-RGMGVILDVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----GGARNIEQIFDNLTAQPHNFTATNPGDVVPY IEAHDNL
                                                                                                                                                       - FTRDSYDSGDWFNRVDYSLQDNNYNVGMPRISDDGSN
TYTAGLIELRRSTNAFTHGTLVDVQANVRLLDIPE
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